C7

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
27 December 2001 (27.12.2001)

PCT

(10) International Publication Number
WO 01/98485 A1

(51) International Patent Classification[7]: C12N 15/11, 15/29, A01H 1/00, 5/00

(21) International Application Number: PCT/NZ01/00115

(22) International Filing Date: 20 June 2001 (20.06.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/598,401 20 June 2000 (20.06.2000) US
09/724,624 28 November 2000 (28.11.2000) US

(71) Applicants *(for all designated States except US)*: **GENESIS RESEARCH & DEVELOPMENT CORPORATION LIMITED** [NZ/NZ]; 1 Fox Street, Parnell, Auckland (NZ). **FLETCHER CHALLENGE FORESTS INDUSTRIES LIMITED** [NZ/NZ]; 585 Great South Road, Penrose, Auckland (NZ).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **PERERA, Ranjan** [LK/US]; 8020 Avenida Navidad #32, San Diego, CA 92122 (US). **RICE, Stephen** [NZ/NZ]; 1/164 Rangitoto Road, Papatoetoe, Auckland (NZ). **EAGLETON, Clare** [NZ/NZ]; 14 Pennycook Place, Pakuranga, Auckland (NZ). **LASHAM, Annette** [GB/NZ]; 12a George Laurenson Lane, Hillsborough, Auckland (NZ).

(74) Agents: **HAWKINS, Michael, Howard** et al.; Baldwin Shelston Waters, P.O. Box 852, Wellington (NZ).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/98485 A1

(54) Title: NUCLEIC ACID SEQUENCES AND METHODS FOR THE MODIFICATION OF PLANT GENE EXPRESSION

(57) Abstract: Novel isolated plant polynucleotide promoter sequences are provided, together with genetic constructs comprising such polynucleotides. Methods for using such constructs in modulating the transcription of DNA sequences of interest are also disclosed, together with transgenic plants comprising such constructs.

Nucleic acid sequences and methods for the modification of plant gene expression

Technical Field of the Invention

This invention relates to the regulation of polynucleotide transcription and/or expression. More specifically, this invention relates to polynucleotide regulatory sequences isolated from plants that are capable of initiating and driving the transcription of polynucleotides, and the use of such regulatory sequences in the modification of transcription of endogenous and/or heterologous polynucleotides and production of polypeptides. Polypeptide sequences are also disclosed.

Background of the Invention

Gene expression is regulated, in part, by the cellular processes involved in transcription. During transcription, a single-stranded RNA complementary to the DNA sequence to be transcribed is formed by the action of RNA polymerases. Initiation of transcription in eukaryotic cells is regulated by complex interactions between *cis*-acting DNA motifs, located within the gene to be transcribed, and *trans*-acting protein factors. Among the *cis*-acting regulatory regions are sequences of DNA, termed promoters, to which RNA polymerase is first bound, either directly or indirectly. As used herein, the term "promoter" refers to the 5' untranslated region of a gene that is associated with transcription and which generally includes a transcription start site. Other cis-acting DNA motifs, such as enhancers, may be situated further up- and/or down-stream from the initiation site.

Both promoters and enhancers are generally composed of several discrete, often redundant elements, each of which may be recognized by one or more *trans*-acting regulatory proteins, known as transcription factors. Promoters generally comprise both proximal and more distant elements. For example, the so-called TATA box, which is important for the binding of regulatory proteins, is generally found about 25 basepairs upstream from the initiation site. The so-called CAAT box is generally found about 75 basepairs upstream of the initiation site. Promoters generally contain between about 100 and 1000 nucleotides, although longer promoter sequences are possible.

For the development of transgenic plants, constitutive promoters that drive strong transgene expression are preferred. Currently, the only available constitutive plant promoter

that is widely used is derived from Cauliflower Mosaic Virus. Furthermore, there exists a need for plant-derived promoters for use in transgenic food plants due to public conceptions regarding the use of viral promoters. Few gymnosperm promoters have been cloned and those derived from angiosperms have been found to function poorly in gymnosperms. There thus remains a need in the art for polynucleotide promoter regions isolated from plants for use in modulating transcription and expression of polynucleotides in transgenic plants.

Summary of the Invention

Briefly, isolated polynucleotide regulatory sequences from eucalyptus and pine that are involved in the regulation of gene expression are disclosed, together with methods for the use of such polynucleotide regulatory regions in the modification of expression of endogenous and/or heterologous polynucleotides in transgenic plants. In particular, the present invention provides polynucleotide promoter sequences from 5' untranslated, or non-coding, regions of plant genes that initiate and regulate transcription of polynucleotides placed under their control, together with isolated polynucleotides comprising such promoter sequences.

In a first aspect, the present invention provides isolated polynucleotide sequences comprising a polynucleotide selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; (b) complements of the sequences recited in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; (c) reverse complements of the sequences recited in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; (d) reverse sequences of the sequences recited in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; (e) sequences having either 40%, 60%, 75% or 90% identical nucleotides, as defined herein, to a sequence of (a) – (d); probes and primers corresponding to the sequences set out in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; polynucleotides comprising at least a specified number of contiguous residues of any of the polynucleotides identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; and extended sequences comprising portions of the sequences set out in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; all of which are referred to herein as "polynucleotides of the present invention." The present invention also provides isolated polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 63-80, 87 and 130; polypeptide variants of those sequences; and polypeptides comprising the isolated polypeptide sequences and variants of those sequences.

In another aspect, the present invention provides genetic constructs comprising a polynucleotide of the present invention, either alone, or in combination with one or more additional polynucleotides of the present invention, or in combination with one or more known polynucleotides, together with cells and target organisms comprising such constructs.

In a related aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a polynucleotide promoter sequence of the present invention, a polynucleotide to be transcribed, and a gene termination sequence. The polynucleotide to be transcribed may comprise an open reading frame of a polynucleotide that encodes a polypeptide of interest, or it may be a non-coding, or untranslated, region of a polynucleotide of interest. The open reading frame may be orientated in either a sense or antisense direction. Preferably, the gene termination sequence is functional in a host plant. Most preferably, the gene termination sequence is that of the gene of interest, but others generally used in the art, such as the *Agrobacterium tumefaciens* nopalin synthase terminator may be usefully employed in the present invention. The genetic construct may further include a marker for the identification of transformed cells.

In a further aspect, transgenic plant cells comprising the genetic constructs of the present invention are provided, together with organisms, such as plants, comprising such transgenic cells, and fruits, seeds and other products, derivatives, or progeny of such plants. Propagules of the inventive transgenic plants are included in the present invention. As used herein, the word "propagule" means any part of a plant that may be used in reproduction or propagation, sexual or asexual, including cuttings.

Plant varieties, particularly registerable plant varieties according to Plant Breeders' Rights, may be excluded from the present invention. A plant need not be considered a "plant variety" simply because it contains stably within its genome a transgene, introduced into a cell of the plant or an ancestor thereof.

In yet another aspect, methods for modifying gene expression in a target organism, such as a plant, are provided, such methods including stably incorporating into the genome of the organism a genetic construct of the present invention. In a preferred embodiment, the target organism is a plant, more preferably a woody plant, most preferably selected from the group consisting of eucalyptus and pine species, most preferably from the group consisting of *Eucalyptus grandis* and *Pinus radiata*.

In another aspect, methods for producing a target organism, such as a plant, having modified polypeptide expression are provided, such methods comprising transforming a plant

cell with a genetic construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

In other aspects, methods for identifying a gene responsible for a desired function or phenotype are provided, the methods comprising transforming a plant cell with a genetic construct comprising a polynucleotide promoter sequence of the present invention operably linked to a polynucleotide to be tested, cultivating the plant cell under conditions conducive to regeneration and mature plant growth to provide a transgenic plant; and comparing the phenotype of the transgenic plant with the phenotype of non-transformed, or wild-type, plants.

In yet a further aspect, the present invention provides isolated polynucleotides that encode ubiquitin. In specific embodiments, the isolated polynucleotides comprise a polynucleotide selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1 and 34; (b) complements of the sequences recited in SEQ ID NO: 1 and 34; (c) reverse complements of the sequences recited in SEQ ID NO: 1 and 34; (d) reverse sequences of the sequence recited in SEQ ID NO: 1 and 34; and (e) sequences having either 40%, 60%, 75% or 90% identical nucleotides, as defined herein, to a sequence of (a) – (d). Polypeptides encoded by such polynucleotides are also provided, together with genetic constructs comprising such polynucleotides, and host cells and transgenic organisms, for example plants, transformed with such genetic constructs. In specific embodiments, such polypeptides comprise a sequence provided in SEQ ID NO: 80 or 67.

In yet further aspects, the present invention provides isolated polynucleotides comprising the DNA sequence of SEQ ID NO: 21, or a complement, reverse complement or variant of SEQ ID NO: 21, together with genetic constructs comprising such polynucleotides and cells transformed with such sequences. As discussed below, removal of the sequence of SEQ ID NO: 21 from a polynucleotide that comprises the sequence of SEQ ID NO: 21 may enhance expression of the polynucleotide. Conversely, the inclusion of the sequence of SEQ ID NO: 21 in a genetic construct comprising a polynucleotide of interest may decrease expression of the polynucleotide.

The above-mentioned and additional features of the present invention and the manner of obtaining them will become apparent, and the invention will be best understood by reference to the following more detailed description. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

Brief Description of the Drawings

Fig. 1 shows the expression in *A. thaliana* of the GUS gene in promoter reporter constructs containing either the superubiquitin promoter with introns, the superubiquitin promoter without introns, or the CaMV 35S promoter. The GUS expression was measured by fluorimetric determination of 4-methyl-umbelliferone (MU) in protein extracts from these plants.

Fig. 2 shows the expression of the GUS gene in tobacco plant protoplasts by deletion constructs containing the superubiquitin promoter with or without the intron. The constructs contained 1,103; 753; 573; 446; 368; and 195 bp upstream of the TATA sequence (bp numbers 1,104-1,110 of SEQ ID NO: 2). The GUS expression was measured by fluorimetric determination of 4-methyl-umbelliferone (MU) in protein extracts from these protoplasts.

Fig. 3 shows the expression of the GUS gene in tobacco plant protoplasts by constructs containing *P. radiata* either the constitutive promoters Elongation factor-1 alpha, 5-adenosylmethionine synthetase or the superubiquitin promoter without the intron. The GUS expression was measured by fluorimetric determination of 4-methyl-umbelliferone (MU) in protein extracts from these protoplasts.

Fig. 4 shows the expression of the GUS gene in tobacco plant protoplasts by a deletion construct containing a fragment of the *E. grandis* constitutive promoter Elongation factor-1 alpha.

Fig. 5 shows the expression in *A. thaliana* of the GUS gene in promoter reporter constructs containing the 3' UTR of the superubiquitin promoter in sense or antisense orientation together with either the superubiquitin promoter with intron, the superubiquitin promoter without intron, or the CaMV 35S promoter. The GUS expression was measured by fluorimetric determination of 4-methyl-umbelliferone (MU) in protein extracts from these plants.

Detailed Description of the Invention

The present invention provides isolated polynucleotide regulatory regions that may be employed in the manipulation of plant phenotypes, together with isolated polynucleotides comprising such regulatory regions. More specifically, polynucleotide promoter sequences isolated from pine and eucalyptus are disclosed. As discussed above, promoters are components of the cellular "transcription apparatus" and are involved in the regulation of

gene expression. Both tissue- and temporal-specific gene expression patterns have been shown to be initiated and controlled by promoters during the natural development of a plant. The isolated polynucleotide promoter sequences of the present invention may thus be employed in the modification of growth and development of plants, and of cellular responses to external stimuli, such as environmental factors and disease pathogens.

Using the methods and materials of the present invention, the amount of a specific polypeptide of interest may be increased or reduced by incorporating additional copies of genes, or coding sequences, encoding the polypeptide, operably linked to an inventive promoter sequence, into the genome of a target organism, such as a plant. Similarly, an increase or decrease in the amount of the polypeptide may be obtained by transforming the target plant with antisense copies of such genes.

The polynucleotides of the present invention were isolated from forestry plant sources, namely from *Eucalyptus grandis* and *Pinus radiata*, but they may alternatively be synthesized using conventional synthesis techniques. Specifically, isolated polynucleotides of the present invention include polynucleotides comprising a sequence selected from the group consisting of sequences identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; complements of the sequences identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; reverse complements of the sequences identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; at least a specified number of contiguous residues (*x*-mers) of any of the above-mentioned polynucleotides; extended sequences corresponding to any of the above polynucleotides; antisense sequences corresponding to any of the above polynucleotides; and variants of any of the above polynucleotides, as that term is described in this specification.

In another embodiment, the present invention provides isolated polypeptides encoded by the polynucleotides of SEQ ID NO: 63-80, 87 and 130.

The polynucleotides and polypeptides of the present invention were putatively identified by DNA and polypeptide similarity searches. In the attached Sequence Listing, SEQ ID NOS. 1-14, 20, 22-62, 81-86 and 88-127 are polynucleotide sequences, and SEQ ID NOS. 63-80, 87 and 130 are polypeptide sequences. The polynucleotides and polypeptides of the present invention have demonstrated similarity to promoters that are known to be involved in regulation of transcription and/or expression in plants. The putative identity of each of the inventive polynucleotides is shown below in Table 1, together with the 5' untranslated region (5' UTR) or putative promoter region (identified by residue number).

TABLE 1

Polynucleotide SEQ ID NO:	Polypeptide SEQ ID NO:	5' UTR	IDENTITY
1	80	1-2064	Super Ubiquitin coding region and UTRs
2	-	1-2064	Super Ubiquitin promoter with intron
3	-	1-1226	Super Ubiquitin promoter without intron
4	-	1-431	Cell division control
5	-	1-167	Xylogenesis – specific
6	-	1-600	4-Coumarate-CoA Ligase (4CL)
7	-	1-591	Cellulose synthase
8	-	1-480	3' end, Cellulose synthase
20	-	1-363	5' end, Cellulose synthase
9	-	1-259	Leaf specific
10	-	1-251	Leaf specific
11	-	1-248	Leaf specific
12	-	1-654	O-methyl transferase
13	-	1-396	Root specific
14	-	1-763	Root specific
22	63	1-406	Pollen coat protein
23	-	1-350	Pollen allergen
24	-	1-49	Pollen allergen
25	64	1-284	Pollen allergen
26	65	1-77	Auxin-induced protein
27	-	1-74	Auxin-induced protein
28	66	1-99	Auxin-induced protein
29	-	1-927	Flower specific
30	-	1-411	Flower specific
31	-	1-178	Flower specific

Polynucleotide SEQ ID NO:	Polypeptide SEQ ID NO:	5' UTR	IDENTITY
32	-	1-178	Flower specific
33	-	1-178	Flower specific
34	67	1-805	Ubiquitin
35	68	1-81	Glyceraldehyde-3-phosphate dehydrogenase
36	69	1-694	Carbonic anhydrase
37	-	1-648	Isoflavone reductase
38	-	1-288	Isoflavone reductase
39	-	1-382	Glyceraldehyde-3-phosphate dehydrogenase
40	70	1-343	Bud specific
41	-	1-313	Xylem-specific
42	-	1-713	Xylem-specific
43	-	1-28	Xylem-specific
44	-	1-35	Xylem-specific
45	71	1-180	Meristem-specific
46	72	1-238	Senescence-like protein
47	-	1-91	Senescence-like protein
48	-	1-91	Senescence-like protein
49	-	1-809	Pollen-specific
50	-	1-428	Pollen-specific
51	73	1-55	Pollen-specific
52	74	1-575	Pollen-specific
53	75	1-35	Pollen-specific
54	-	1-335	Nodulin homolog pollen specific
55	-	1-336	Nodulin homolog pollen specific
56	76	1-157	Sucrose synthase
57	77	1-446	Sucrose synthase
58	-	1-326	Sucrose synthase

Polynucleotide SEQ ID NO:	Polypeptide SEQ ID NO:	5' UTR	IDENTITY
59	-	1-311	Flower specific
60	78	1-694	O-methyl transferase
61	79	1-112	Elongation factor A
62	-	1-420	Elongation factor A
81	-	-	MIF homologue
82	-	-	MIF homologue
83	-	-	MIF homologue
84	-	-	MIF homologue
85	-	-	MIF homologue
86	87	1-87	MIF homologue
88	-	1-1156	Chalcone synthase
89	-	1-2590	Unknown flower specific
90	-	1-1172	Unknown flower specific
91	-	1-446	Sucrose synthase
92	-	1-2119	Unknown xylem specific
93	-	1-2571	Glyceraldehyde-3-Phosphate dehydrogenase
94	-	1-1406	Unknown pollen specific
95	-	1-2546	*Pinus radiata* male-specific protein (PrMALE1)
96	-	1-4726	*Pinus radiata* male-specific protein (PrMALE1)
97	-	1-635	UDP glucose glycosyltransferase
98	-	1-468	Elongation Factor A1
99	-	1-222	Elongation Factor A1
100	-	1-410	S-adenosylmethionine synthetase
101	-	1-482	S-adenosylmethionine synthetase
102	-	1-230	S-adenosylmethionine synthetase
103	-	1-596	UDP glucose 6 dehydrogenase
104	-	1-653	Hypothetical protein

Polynucleotide SEQ ID NO:	Polypeptide SEQ ID NO:	5' UTR	IDENTITY
105	-	1-342	Laccase 1
106	-	1-342	Laccase 1
106	-	1-948	Arabinogalactan-like 1
108	-	1-362	Arabinogalactan-like 2
109	-	1-326	Arabinogalactan like-2
110	-	1-296	Root Receptor-like kinase
111	-	1-723	Root Receptor-like kinase
112	-	1-1301	*Pinus radiata* Lipid Transfer Protein 2 (PrLTP2)
113	-	1-1668	Caffeic acid O-methyltransferase
114	-	1-850	UDP glucose glycosyltransferase
115	-	1-986	UDP glucose 6 dehydrogenase
116	-	1-947	Laccase 1
117	-	1-1766	Arabinogalactan like-1
118	-	1-1614	Constans
119	-	1-602	Flowering Promoting Factor 1 (FPF1)
120	-	1-901	Agamous
121	-	1-1,245	Dreb 1A Transcription factor
122	-	1-959	Drought Induced Protein 19
123	-	1-1,140	Salt Tolerance protein
124	130	1-887	Low Temperature Induced LTI-16
125	-	1-1,243	Xylem specific receptor-like kinase
126	-	1-1,047	Root specific
127	-	1-3,552	Elongation Factor 1-alpha

In one embodiment, the present invention provides polynucleotide sequences isolated from *Pinus radiata* and *Eucalyptus grandis* that encode a ubiquitin polypeptide. The full-length sequence of the ubiquitin polynucleotide isolated from *Pinus radiata* is provided in SEQ ID NO: 1, with the sequence of the promoter region including an intron being provided

in SEQ ID NO: 2 and the sequence of the promoter region excluding the intron being provided in SEQ ID NO: 3. The sequence of the ubiquitin polynucleotide isolated from *Eucalyptus grandis* is provided in SEQ ID NO: 34. In a related embodiment, the present invention provides isolated polypeptides encoded by the isolated polynucleotides of SEQ ID NO: 1 and 34, including polypeptides comprising the sequences of SEQ ID NO: 80 and 67.

The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all such operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion *et al.* "Antisense techniques," *Methods in Enzymol.* 254(23):363-375, 1995; and Kawasaki *et al.*, in *Artific. Organs* 20(8):836-848, 1996.

All of the polynucleotides and polypeptides described herein are isolated and purified, as those terms are commonly used in the art. Preferably, the polypeptides and polynucleotides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

The definition of the terms "complement", "reverse complement" and "reverse sequence", as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement and reverse sequence are as follows:

Complement	3' TCCTGG 5'
Reverse complement	3' GGTCCT 5'
Reverse sequence	5' CCAGGA 3'

Some of the polynucleotides of the present invention are "partial" sequences, in that they do not represent a full-length gene encoding a full-length polypeptide. Such partial sequences may be extended by analyzing and sequencing various DNA libraries using primers and/or probes and well known hybridization and/or PCR techniques. Partial

sequences may be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as "corresponding to" a sequence identified as one of the sequences of SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or a variant thereof, or a portion of one of the sequences of SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or a variant thereof, when the extended polynucleotide comprises an identified sequence or its variant, or an identified contiguous portion (*x*-mer) of one of the sequences of SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or a variant thereof. Such extended polynucleotides may have a length of from about 50 to about 4,000 nucleic acids or base pairs, and preferably have a length of less than about 4,000 nucleic acids or base pairs, more preferably yet a length of less than about 3,000 nucleic acids or base pairs, more preferably yet a length of less than about 2,000 nucleic acids or base pairs. Under some circumstances, extended polynucleotides of the present invention may have a length of less than about 1,800 nucleic acids or base pairs, preferably less than about 1,600 nucleic acids or base pairs, more preferably less than about 1,400 nucleic acids or base pairs, more preferably yet less than about 1,200 nucleic acids or base pairs, and most preferably less than about 1,000 nucleic acids or base pairs.

Similarly, RNA sequences, reverse sequences, complementary sequences, antisense sequences, and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127.

The polynucleotides identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, and their extensions, may contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides. Additionally, open reading frames encoding polypeptides may be identified in extended or full length sequences corresponding to the sequences set out as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis include, for example, "GeneWise", available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; "Diogenes", available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43, Minneapolis MN 55455 and "GRAIL", available from the Informatics

Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Open reading frames and portions of open reading frames may be identified in the polynucleotides of the present invention. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified. Thus, open reading frames encoding polypeptides may be identified using the polynucleotides of the present invention.

Once open reading frames are identified in the polynucleotides of the present invention, the open reading frames may be isolated and/or synthesized. Expressible genetic constructs comprising the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art, may then be constructed. Such genetic constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells, including plant cells, mammalian cells, bacterial cells, algae and the like.

Polypeptides encoded by the polynucleotides of the present invention may be expressed and used in various assays to determine their biological activity. Such polypeptides may be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

The term "polypeptide", as used herein, encompasses amino acid chains of any length including full length proteins, wherein amino acid residues are linked by covalent peptide bonds. Polypeptides of the present invention may be isolated and purified natural products, or may be produced partially or wholly using recombinant techniques. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a nucleotide sequence which includes the partial isolated DNA sequences of the present invention.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having a sequence selected from the group consisting of sequences provided in SEQ ID NO: 63-80, 87 and 130, and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using, for example, the representative assays provided below. A functional portion comprising an active site may be made up of separate portions present on one or more polypeptide chains and generally exhibits high substrate specificity.

Portions and other variants of the inventive polypeptides may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, wherein amino acids are sequentially added to a growing amino acid chain. (Merrifield, *J. Am. Chem. Soc.* 85: 2149-2154, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer / Applied Biosystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82: 488-492, 1985). Sections of DNA sequences may also be removed using standard techniques to permit preparation of truncated polypeptides.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 50%, more preferably at least 75%, and most preferably at least 90% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotide and polypeptide sequences may be aligned, and percentage of identical residues in a specified region may be determined against other polynucleotide and polypeptide sequences, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The similarity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN algorithm Version 2.0.4 [Feb-24-1998], Version 2.0.6 [Sept-16-1998] and Version 2.0.11 [Jan-20-2000], set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP, and BLASTX, is described in the publication of Altschul, *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res.* 25: 3389-3402, 1997. The BLASTN software is available on the NCBI anonymous FTP server (ftp://ncbi.nlm.nih.gov) under /blast/executables/ and is available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894 USA.

The FASTA software package is available from the University of Virginia (University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025). Version 2.0u4, February 1996, set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson and Lipman, "Improved Tools for Biological Sequence Analysis," *Proc. Natl. Acad. Sci. USA* 85: 2444-2448, 1988; and Pearson, "Rapid and Sensitive Sequence Comparison with FASTP and FASTA," *Methods in Enzymol.* 183: 63-98, 1990.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotide sequences: Unix running command: blastall -p blastn -d embldb -e 10 –G0 -E0 -r 1 -v 30 -b 30 -i queryseq –o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes

default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; and -o BLAST report Output File [File Out] Optional.

The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity of polypeptide sequences: blastall –p blastp –d swissprotdb –e 10 -G 0 -E 0 –v 30 –b 30 –i queryseq –o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, FASTA, BLASTP or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

The BLASTN, FASTA and BLASTP algorithms also produce "Expect" values for alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database, such as the preferred EMBL database, indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the polynucleotide sequences then have a probability of 90% of being the same. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN or FASTA algorithm.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or

less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN, FASTA, or BLASTP algorithms set at parameters described above. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or FASTA algorithms set at parameters described above. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being the same as a polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the parameters described above.

Alternatively, variant polynucleotides of the present invention hybridize to the polynucleotide sequences recited in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or complements, reverse sequences, or reverse complements of those sequences under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65° C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar activity to a polypeptide encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or complements, reverse sequences, or reverse complements thereof, as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or complements, reverse complements or reverse sequences thereof, as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NO: 63-80, 87 and 130, as a result of amino

acid substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by an encompassed within the present invention. In certain embodiments, variants of the inventive polypeptides and polynucleotides possess biological activities that are the same or similar to those of the inventive polypeptides or polynucleotides. Such variant polynucleotides function as promoter sequences and are thus capable of modifying gene expression in a plant.

The polynucleotides of the present invention may be isolated from various libraries, or may be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (*e.g.*, Beckman Oligo 1000M DNA Synthesizer) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5-nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5-nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

Polynucleotides of the present invention also comprehend polynucleotides comprising at least a specified number of contiguous residues (x-mers) of any of the polynucleotides identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, complements, reverse sequences, and reverse complements of such sequences, and their variants. Similarly, polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (x-mers) of any of the polypeptides identified as SEQ ID NO: 63-80, 87 and 130, and their variants. As used herein, the term "x-mer," with reference to a specific value of "x," refers to a sequence comprising at least a specified number ("x") of contiguous residues of any of the polynucleotides identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or the polypeptides identified as SEQ ID NO: 63-80, 87 and 130. According to preferred embodiments, the value of x is preferably at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides and polypeptides of the present invention comprise a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, a 300-

mer, 400-mer, 500-mer or 600-mer of a polynucleotide or polypeptide identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, and variants thereof.

As noted above, the inventive polynucleotide promoter sequences may be employed in genetic constructs to drive transcription and/or expression of a polynucleotide of interest. The polynucleotide of interest may be either endogenous or heterologous to an organism, for example a plant, to be transformed. The inventive genetic constructs may thus be employed to modulate levels of transcription and/or expression of a polynucleotide, for example gene, that is present in the wild-type plant, or may be employed to provide transcription and/or expression of a DNA sequence that is not found in the wild-type plant.

In certain embodiments, the polynucleotide of interest comprises an open reading frame that encodes a target polypeptide. The open reading frame is inserted in the genetic construct in either a sense or antisense orientation, such that transformation of a target plant with the genetic construct will lead to a change in the amount of polypeptide compared to the wild-type plant. Transformation with a genetic construct comprising an open reading frame in a sense orientation will generally result in over-expression of the selected polypeptide, while transformation with a genetic construct comprising an open reading frame in an antisense orientation will generally result in reduced expression of the selected polypeptide. A population of plants transformed with a genetic construct comprising an open reading frame in either a sense or antisense orientation may be screened for increased or reduced expression of the polypeptide in question using techniques well known to those of skill in the art, and plants having the desired phenotypes may thus be isolated.

Alternatively, expression of a target polypeptide may be inhibited by inserting a portion of the open reading frame, in either sense or antisense orientation, in the genetic construct. Such portions need not be full-length but preferably comprise at least 25 and more preferably at least 50 residues of the open reading frame. A much longer portion or even the full length DNA corresponding to the complete open reading frame may be employed. The portion of the open reading frame does not need to be precisely the same as the endogenous sequence, provided that there is sufficient sequence similarity to achieve inhibition of the target gene. Thus a sequence derived from one species may be used to inhibit expression of a gene in a different species.

In further embodiments, the inventive genetic constructs comprise a polynucleotide including an untranslated, or non-coding, region of a gene coding for a target polypeptide, or a polynucleotide complementary to such an untranslated region. Examples of untranslated

regions which may be usefully employed in such constructs include introns and 5'-untranslated leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of the polypeptide expressed in the plant by the process of cosuppression, in a manner similar to that discussed, for example, by Napoli *et al.*, *Plant Cell* 2:279-290, 1990 and de Carvalho Niebel *et al.*, *Plant Cell* 7:347-358, 1995.

Alternatively, regulation of polypeptide expression can be achieved by inserting appropriate sequences or subsequences (e.g. DNA or RNA) in ribozyme constructs (McIntyre and Manners, *Transgenic Res.* 5(4):257-262, 1996). Ribozymes are synthetic RNA molecules that comprise a hybridizing region complementary to two regions, each of which comprises at least 5 contiguous nucleotides in a mRNA molecule encoded by one of the inventive polynucleotides. Ribozymes possess highly specific endonuclease activity, which autocatalytically cleaves the mRNA.

The polynucleotide of interest, such as a coding sequence, is operably linked to a polynucleotide promoter sequence of the present invention such that a host cell is able to transcribe an RNA from the promoter sequence linked to the polynucleotide of interest. The polynucleotide promoter sequence is generally positioned at the 5' end of the polynucleotide to be transcribed. Use of a constitutive promoter, such as the *Pinus radiata* ubiquitin polynucleotide promoter sequence of SEQ ID NO: 2 and 3' or the *Eucalyptus grandis* ubiquitin polynucleotide promoter sequence contained within SEQ ID NO: 34, will affect transcription of the polynucleotide of interest in all parts of the transformed plant. Use of a tissue specific promoter, such as the leaf-specific promoters of SEQ ID NO: 9-11, the root-specific promoters of SEQ ID NO: 13 and 14, the flower-specific promoters of SEQ ID NO: 29-33, 59 and 89-90, the pollen-specific promoters of SEQ ID NO: 49-55 and 94, the bud-specific promoter of SEQ ID NO: 40 or the meristem-specific promoter of SEQ ID NO: 45, will result in production of the desired sense or antisense RNA only in the tissue of interest. Temporally regulated promoters, such as the xylogenesis-specific promoters of SEQ ID NO: 5, 41-44 and 92, can be employed to effect modulation of the rate of DNA transcription at a specific time during development of a transformed plant. With genetic constructs employing inducible gene promoter sequences, the rate of DNA transcription can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like.

The inventive genetic constructs further comprise a gene termination sequence which is located 3' to the polynucleotide of interest. A variety of gene termination sequences which

may be usefully employed in the genetic constructs of the present invention are well known in the art. One example of such a gene termination sequence is the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. The gene termination sequence may be endogenous to the target plant or may be exogenous, provided the promoter is functional in the target plant. For example, the termination sequence may be from other plant species, plant viruses, bacterial plasmids and the like.

The genetic constructs of the present invention may also contain a selection marker that is effective in cells of the target organism, such as a plant, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer resistance to one or more toxins. One example of such a marker is the NPTII gene whose expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers *et al.*, *in* Weissbach A and H, eds. *Methods for Plant Molecular Biology*, Academic Press Inc.: San Diego, CA, 1988). Transformed cells can thus be identified by their ability to grow in media containing the antibiotic in question. Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots.

Techniques for operatively linking the components of the inventive genetic constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, (*Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989). The genetic construct of the present invention may be linked to a vector having at least one replication system, for example *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced and the correctness of the manipulation determined.

The genetic constructs of the present invention may be used to transform a variety of target organisms including, but not limited to, plants. Plants which may be transformed using the inventive constructs include both monocotyledonous angiosperms (*e.g.*, grasses, corn, grains, oat, wheat and barley) and dicotyledonous angiosperms (*e.g.*, *Arabidopsis*, tobacco, legumes, alfalfa, oaks, eucalyptus, maple), and Gymnosperms (*e.g.*, Scots pine; *see* Aronen, *Finnish Forest Res. Papers*, Vol. 595, 1996), white spruce (Ellis *et al.*, *Biotechnology* 11:84-89, 1993), and larch (Huang *et al.*, *In Vitro Cell* 27:201-207, 1991). In a preferred embodiment, the inventive genetic constructs are employed to transform woody plants, herein defined as a tree or shrub whose stem lives for a number of years and increases in diameter

each year by the addition of woody tissue. Preferably the target plant is selected from the group consisting of eucalyptus and pine species, most preferably from the group consisting of *Eucalyptus grandis* and *Pinus radiata*. Other species which may be usefully transformed with the genetic constructs of the present invention include, but are not limited to: pines such as *Pinus banksiana, Pinus brutia, Pinus caribaea, Pinus clausa, Pinus contorta, Pinus coulteri, Pinus echinata, Pinus eldarica, Pinus ellioti, Pinus jeffreyi, Pinus lambertiana, Pinus monticola, Pinus nigra, Pinus palustrus, Pinus pinaster, Pinus ponderosa, Pinus resinosa, Pinus rigida, Pinus serotina, Pinus strobus, Pinus sylvestris, Pinus taeda, Pinus virginiana*; other gymnosperms, such as *Abies amabilis, Abies balsamea, Abies concolor, Abies grandis, Abies lasiocarpa, Abies magnifica, Abies procera, Chamaecyparis lawsoniona, Chamaecyparis nootkatensis, Chamaecyparis thyoides, Huniperus virginiana, Larix decidua, Larix laricina, Larix leptolepis, Larix occidentalis, Larix siberica, Libocedrus decurrens, Picea abies, Picea engelmanni, Picea glauca, Picea mariana, Picea pungens, Picea rubens, Picea sitchensis, Pseudotsuga menziesii, Sequoia gigantea, Sequoia sempervirens, Taxodium distichum, Tsuga canadensis, Tsuga heterophylla, Tsuga mertensiana, Thuja occidentalis, Thuja plicata*; and Eucalypts, such as *Eucalyptus alba, Eucalyptus bancroftii, Eucalyptus botyroides, Eucalyptus bridgesiana, Eucalyptus calophylla, Eucalyptus camaldulensis, Eucalyptus citriodora, Eucalyptus cladocalyx, Eucalyptus coccifera, Eucalyptus curtisii, Eucalyptus dalrympleana, Eucalyptus deglupta, Eucalyptus delagatensis, Eucalyptus diversicolor, Eucalyptus dunnii, Eucalyptus ficifolia, Eucalyptus globulus, Eucalyptus gomphocephala, Eucalyptus gunnii, Eucalyptus henryi, Eucalyptus laevopinea, Eucalyptus macarthurii, Eucalyptus macrorhyncha, Eucalyptus maculata, Eucalyptus marginata, Eucalyptus megacarpa, Eucalyptus melliodora, Eucalyptus nicholii, Eucalyptus nitens, Eucalyptus nova-anglica, Eucalyptus obliqua, Eucalyptus obtusiflora, Eucalyptus oreades, Eucalyptus pauciflora, Eucalyptus polybractea, Eucalyptus regnans, Eucalyptus resinifera, Eucalyptus robusta, Eucalyptus rudis, Eucalyptus saligna, Eucalyptus sideroxylon, Eucalyptus stuartiana, Eucalyptus tereticornis, Eucalyptus torelliana, Eucalyptus urnigera, Eucalyptus urophylla, Eucalyptus viminalis, Eucalyptus viridis, Eucalyptus wandoo* and *Eucalyptus youmanni*; and hybrids of any of these species.

Techniques for stably incorporating genetic constructs into the genome of target plants are well known in the art and include *Agrobacterium tumefaciens* mediated introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of

technique will depend upon the target plant to be transformed. For example, dicotyledonous plants and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid technology, as described, for example by Bevan, *Nucleic Acids Res.* 12:8711-8721, 1984. Targets for the introduction of the genetic constructs of the present invention include tissues, such as leaf tissue, dissociated cells, protoplasts, seeds, embryos, meristematic regions; cotyledons, hypocotyls, and the like. The preferred method for transforming eucalyptus and pine is a biolistic method using pollen (see, for example, Aronen, *Finnish Forest Res. Papers*, Vol. 595, 53pp, 1996) or easily regenerable embryonic tissues.

Once the cells are transformed, cells having the inventive genetic construct incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the case of seeds or embryos, an appropriate germination or callus initiation medium is employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. For a review of regeneration of forest trees see Dunstan *et al.*, "Somatic embryogenesis in woody plants," *in* Thorpe TA, ed., *In Vitro Embryogenesis of Plants* (*Current Plant Science and Biotechnology in Agriculture Vol. 20*), Chapter 12, pp. 471-540, 1995. Specific protocols for the regeneration of spruce are discussed by Roberts *et al.*, "Somatic embryogenesis of spruce," *in* Redenbaugh K, ed., *Synseed: applications of synthetic seed to crop improvement,* CRC Press: Chapter 23, pp. 427-449, 1993). Transformed plants having the desired phenotype may be selected using techniques well known in the art. The resulting transformed plants may be reproduced sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

As discussed above, the production of RNA in target cells can be controlled by choice of the promoter sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target host. A target organism may be transformed with more than one genetic construct of the present invention, thereby modulating the activity of more than gene. Similarly, a genetic construct may be assembled containing more than one open reading frame coding for a polypeptide of interest or more than one untranslated region of a gene coding for such a polypeptide.

The isolated polynucleotides of the present invention also have utility in genome mapping, in physical mapping, and in positional cloning of genes. As detailed below, the

polynucleotide sequences identified as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, and their variants, may be used to design oligonucleotide probes and primers. Oligonucleotide probes designed using the polynucleotides of the present invention may be used to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the polynucleotides of the present invention may also be used in connection with various microarray technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

As used herein, the term "oligonucleotide" refers to a relatively short segment of a polynucleotide sequence, generally comprising between 6 and 60 nucleotides, and comprehends both probes for use in hybridization assays and primers for use in the amplification of DNA by polymerase chain reaction.

An oligonucleotide probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or a variant, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127, or a variant of one of the specified sequences. Oligonucleotide probes and primers of the present invention are substantially complementary to a polynucleotide disclosed herein.

Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95% and more preferably at least 98% to 100% of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a second DNA strand under stringent hybridization conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM, and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C, and most preferably greater than about 37°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as probe composition,

presence of organic solvents and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone.

In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length or, preferably from about 10 to 50 base pairs in length or, more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, and potential for formation of loops and other factors, which are well known in the art.. Preferred techniques for designing PCR primers are disclosed in Dieffenbach, CW and Dyksler, GS. *PCR Primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995. A software program suitable for designing probes, and especially for designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504.

A plurality of oligonucleotide probes or primers corresponding to a polynucleotide of the present invention may be provided in a kit form. Such kits generally comprise multiple DNA or oligonucleotide probes, each probe being specific for a polynucleotide sequence. Kits of the present invention may comprise one or more probes or primers corresponding to a polynucleotide of the present invention, including a polynucleotide sequence identified in SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-120.

In one embodiment useful for high-throughput assays, the oligonucleotide probe kits of the present invention comprise multiple probes in an array format, wherein each probe is immobilized at a predefined, spatially addressable location on the surface of a solid substrate. Array formats which may be usefully employed in the present invention are disclosed, for example, in U.S. Patents No. 5,412,087 and 5,545,451; and PCT Publication No. WO 95/00450, the disclosures of which are hereby incorporated by reference.

The polynucleotides of the present invention may also be used to tag or identify an organism or reproductive material therefrom. Such tagging may be accomplished, for example, by stably introducing a non-disruptive non-functional heterologous polynucleotide identifier into an organism, the polynucleotide comprising one of the polynucleotides of the present invention.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Isolation and Characterization of a Ubiquitin Gene Promoter from *Pinus radiata*

Pinus radiata cDNA expression libraries were constructed and screened as follows. mRNA was extracted from plant tissue using the protocol of Chang *et al.*, *Plant Molecular Biology Reporter* 11:113-116, 1993 with minor modifications. Specifically, samples were dissolved in CPC-RNAXB (100 mM Tris-Cl, pH 8,0; 25 mM EDTA; 2.0 M NaCl; 2%CTAB; 2% PVP and 0.05% Spermidine*3HCl) and extracted with chloroform:isoamyl alcohol, 24:1. mRNA was precipitated with ethanol and the total RNA preparate was purified using a Poly(A) Quik mRNA Isolation Kit (Stratagene, La Jolla, CA). A cDNA expression library was constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA clones in Lambda ZAP using a ZAP Express cDNA Synthesis Kit (Stratagene), according to the manufacturer's protocol. The resulting cDNAs were packaged using a Gigapack II Packaging Extract (Stratagene) employing 1 µl of sample DNA from the 5 µl ligation mix. Mass excision of the library was done using XL1-Blue MRF' cells and XLOLR cells (Stratagene) with ExAssist helper phage (Stratagene). The excised phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing X-gal and isopropylthio-beta-galactoside (IPTG).

Of the colonies plated and picked for DNA miniprep, 99% contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and cDNA was purified by means of alkaline lysis and polyethylene glycol (PEG) precipitation. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye primer sequences were prepared using a Turbo Catalyst 800 machine (Perkin Elmer/Applied Biosystems Division, Foster City, CA) according to the manufacturer's protocol.

DNA sequence for positive clones was obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced first from the 5' end and, in some cases, also from the 3' end. For some clones, internal sequence was obtained using subcloned fragments. Subcloning was performed using standard procedures of restriction mapping and subcloning to pBluescript II SK+ vector.

As described below, one of the most abundant sequences identified was a ubiquitin gene, hereinafter referred to as the "Super-Ubiquitin or SU" gene.

Isolation of cDNA clones containing the ubiquitin gene

Sequences of cDNA clones with homology to the ubiquitin gene were obtained from high-throughput cDNA sequencing as described above. Sequences from several independent clones were assembled in a contig and a consensus sequence was generated from overlapping clones. The determined nucleotide sequence of the isolated Super Ubiquitin clone, comprising the promoter region (including an intron), coding region and 3' untranslated region (UTR) is provided in SEQ ID NO: 1. The 5' UTR is represented by residues 1 to 2,064, the intron by residues 1,196 to 2,033, and the coding region of the gene, which contains three direct repeats, by residues 2,065 to 2,751. The 3' UTR is 328 residues long (residues 2,755 to 3,083). The nucleotide sequence of the Super Ubiquitin promoter region only, including the intron, is given in SEQ ID NO: 2. The nucleotide sequence of the Super Ubiquitin promoter region only, excluding the intron, is given in SEQ ID NO: 3. The predicted amino acid sequence for the *Pinus radiata* Super Ubiquitin is provided in SEQ ID NO: 80.

Ubiquitin proteins function as part of a protein degradation pathway, in which they covalently attach to proteins, thereby targeting them for degradation (for a review, see Belknap and Garbarino, *Trends in Plant Sciences* 1:331-335, 1996). The protein is produced from a precursor polypeptide, encoded by a single mRNA. The Super Ubiquitin mRNA contains three copies of the ubiquitin monomer.

Cloning of the Super Ubiquitin Promoter

Fragments of the Super Ubiquitin promoter were cloned by two different PCR-based approaches.

Method 1: Long Distance Gene Walking PCR

Using "Long Distance Gene Walking" PCR (Min and Powell, *Biotechniques* 24:398-400, 1998), a 2 kb fragment was obtained that contained the entire coding region of the ubiquitin gene, a 900 bp intron in the 5' UTR and approximately 100 bp of the promoter.

To generate this fragment, 2 nested primers were designed from the 3' UTR of the Super Ubiquitin cDNA sequence isolated from pine. Generally, the 5' UTR is used for

primer design to amplify upstream sequence. However, the available 5' UTR of Super Ubiquitin was very short, and two initial primers derived from this region failed to amplify any fragments. Therefore, the primers of SEQ ID NO: 15 and 16 were designed from the 3' UTR.

The method involved an initial, linear PCR step with pine genomic DNA as template using the primer of SEQ ID NO: 15, and subsequent C-tailing of the single stranded DNA product using terminal transferase. The second PCR-step used these fragments as template for amplification with the primer of SEQ ID NO: 16 and primer AP of SEQ ID NO: 17. The AP primer was designed to bind to the polyC tail generated by the terminal transferase. Both primers (SEQ ID NO: 16 and 17) contained a 5'-*Not*I restriction site for the cloning of products into the *Not*I site of a suitable vector. The final PCR product contained fragments of different sizes. These fragments were separated by electrophoresis and the largest were purified from the gel, digested with restriction endonuclease *Not*I and cloned in the *Not*I site of expression vector pBK-CMV (Stratagene, La Jolla, CA). The largest of these clones contained the complete coding region of the gene (no introns were found in the coding sequence) and a 5' UTR which contained a 900 bp intron.

Method 2: "Genome Walker" kit

The Super Ubiquitin gene promoter was cloned using a "Genome Walker" kit (Clontech, Palo Alto, CA). This is also a PCR-based method, which requires two PCR primers to be constructed, one of which must be gene-specific. Although the ubiquitin coding region is highly conserved, the 5' UTR from different ubiquitin genes is not conserved and could therefore be used to design a gene-specific primer. A 2.2 kb fragment was amplified and subcloned in pGEM-T-easy (Promega, Madison, WI). Analysis by PCR and DNA sequencing showed that the clone contained 5' UTR sequence of the Super Ubiquitin gene, including the 900 bp intron and approximately 1 kb of putative promoter region. An intron in the 5' UTR is a common feature of plant polyubiquitin genes and may be involved in determining gene expression levels.

The gene specific primers used for these PCR reactions are provided in SEQ ID NO: 18 and 19.

Expression of Super Ubiquitin

Using primers derived from the gene-specific 5' and 3' UTR sequences, expression levels of Super Ubiquitin in different plant tissues was examined by means of RT-PCR. Super Ubiquitin was found to be expressed in all plant tissues examined, including branch phloem and xylem, feeder roots, fertilized cones, needles, one year old cones, pollen sacs, pollinated cones, root xylem, shoot buds, structural roots, trunk phloem and trunk. Expression of Super Ubiquitin in plant tissues was also demonstrated in a Northern blot assay using a PCR probe prepared from the 5'UTR.

Functional analysis of the Super Ubiquitin Promoter

To test the function of the Super Ubiquitin promoter in plants, *Arabidopsis thaliana* was transformed with constructs containing the reporter gene for Green Fluorescent Protein (GFP) operably linked to either the Super Ubiquitin promoter of SEQ ID NO: 2 or SEQ ID NO: 3 (i.e., either with or without the intron). Constructs lacking a promoter were used as a negative control, with a plant T-DNA vector carrying a CaMV 35S promoter cloned in front of GFP being used as a positive control. The constructs were introduced into *Arabidopsis* via *Agrobacterium*-mediated transformation.

All the plant culture media were according to the protocol of Valvekens and Van Montagu, *Proc. Natl. Acad. Sci. USA* 85:5536-5540, 1988 with minor modifications. For root transformation, sterilized seeds were placed in a line on the surface of germination medium, the plates were placed on their sides to facilitate root harvesting, and the seeds were grown for two weeks at 24°C with a 16 h photoperiod.

Expression of the constructs was measured by determining expression levels of the reporter gene for Green Fluorescent Protein (GFP). Preliminary GFP expression (transient) was detected in early transgenic roots during T-DNA transfer. Transgenic roots that developed green callus, growing on shoot-inducing medium containing 50 µg/ml Kanamycin and 100 µg/ml Timentin, were further tested for GFP expression. After several weeks of stringent selection on Kanamycin medium, several independent transgenic *Arabidopsis* lines were engineered and tested for GFP expression.

Expression was seen both with the Super Ubiquitin promoter including intron and the Super Ubiquitin promoter without the intron. However, preliminary results indicated that the levels of expression obtained with the Super Ubiquitin intron-less promoter construct were

significantly higher than those seen with the promoter including intron, suggesting that the intron may contain a repressor. The sequence of the intron is provided in SEQ ID NO: 21.

EXAMPLE 2

Isolation of a CDC Promoter from *Pinus radiata*

Plant polynucleotide sequences homologous to the Cell Division Control (CDC) protein gene were isolated from a *Pinus radiata* cDNA expression library as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, 5'UTR sequence containing the putative promoter of the *P. radiata* CDC gene was isolated from genomic DNA. The determined nucleotide sequence is given in SEQ ID NO: 4.

EXAMPLE 3

Isolation of a Xylogenesis-Specific Promoter from *Pinus radiata*

Plant polynucleotide sequences specific for plant xylogenesis were isolated from *Pinus radiata* cDNA expression libraries prepared from xylem, essentially as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, sequences containing putative *Pinus radiata* xylogenesis-specific promoters were isolated from genomic DNA. The determined nucleotide sequences are provided in SEQ ID NO: 5 and 41-44. An extended cDNA sequence for the clone of SEQ ID NO: 41-44 is provided in SEQ ID NO: 92.

EXAMPLE 4

Isolation of a 4-Coumarate-CoA Ligase Promoter from *Pinus radiata*

Plant polynucleotide sequences homologous to the 4-Coumarate-CoA Ligase (4CL) gene were isolated from a *Pinus radiata* cDNA expression library as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, sequences containing the putative promoter of the *P. radiata* 4CL gene was isolated from genomic DNA. The determined nucleotide sequence is given in SEQ ID NO: 6.

Genetic constructs comprising the reporter gene for Green Fluorescent Protein (GFP) or GUS reporter genes operably linked to the promoter of SEQ ID NO: 6 were prepared and used to transform *Arabidopsis thaliana* plants.

EXAMPLE 5

Isolation of a Cellulose Synthase Promoter from *Eucalyptus grandis*

Plant polynucleotide sequences homologous to the cellulose synthase gene were isolated from a *Eucalyptus grandis* cDNA expression library essentially as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, 5'UTR sequences containing the putative promoter of the *E. grandis* cellulose synthase gene were isolated from genomic DNA. Independent PCR experiments using different DNA bands as templates yielded two sequences which contained a number of base differences. One band was 750 bp in length and the nucleotide sequence of this band is given in SEQ ID NO: 7. The other band was 3 kb in length. The sequence of the 3' end of this band corresponded to the sequence given in SEQ ID NO: 7, with a number of base pair differences. The sequence of this 3' end is given in SEQ ID NO: 8. The sequence of the 5' end of this band is given in SEQ ID NO: 20.

EXAMPLE 6

Isolation of a Leaf-Specific Promoter from *Eucalyptus grandis*

Plant polynucleotide sequences specific for leaf were isolated from *Eucalyptus grandis* cDNA expression libraries prepared from leaf tissue, essentially as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, 5'UTR sequence containing a leaf-specific promoter of a novel *E. grandis* gene (of unknown function) was isolated from genomic DNA. Independent PCR experiments using different DNA bands as templates yielded three sequences which contained a number of base differences and deletions. The determined nucleotide sequences of the three PCR fragments are given in SEQ ID NO: 9-11.

EXAMPLE 7

Isolation of an O-Methyl Transferase Promoter from *Eucalyptus grandis*

Plant polynucleotide sequences homologous to an O-methyl transferase (OMT) gene were isolated from a *Eucalyptus grandis* cDNA expression library essentially as described in

Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, 5'UTR sequences containing the putative promoter of the *E. grandis* OMT gene was isolated from genomic DNA. The determined nucleotide sequence is given in SEQ ID NO: 12. This promoter sequence was extended by further sequencing. The extended cDNA sequences are given in SEQ ID NO: 60 and 113.

Genetic constructs comprising the reporter gene for Green Fluorescent Protein (GFP) operably linked to the promoter of SEQ ID NO: 12 were prepared and used to transform *Arabidopsis thaliana.*

EXAMPLE 8

Isolation of Root-Specific Promoters from *Pinus radiata*

Plant polynucleotide sequences homologous to the root-specific receptor-like kinase gene were isolated from a *Pinus radiata* cDNA expression library as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, 5'UTR sequence containing a putative *P. radiata* root-specific promoter was isolated from genomic DNA. Two independent PCR experiments yielded sequences that contained a number of base differences. The determined nucleotide sequences from the two experiments are given in SEQ ID NO: 13, 14, 110 and 111.

EXAMPLE 9

Isolation of an EF1-alpha Promoter from *Eucalyptus Grandis*

Plant polynucleotide sequences homologous to the *Eucalyptus* Elongation Factor-alpha (EF1-alpha) gene were isolated from a *Eucalyptus grandis* cDNA expression library and used to screen a *Eucalyptus grandis* genomic DNA library as follows.

The *Eucalyptus grandis* genomic DNA library was constructed using genomic DNA extracted from *Eucalyptus nitens x grandis* plant tissue, according to the protocol of Doyle and Doyle, *Focus* 12:13-15, 1990, with minor modifications. Specifically, plant tissue was ground under liquid nitrogen and dissolved in 2X CTAB extraction buffer (2% CTAB, hexadecyltrimethylammonium bromide; 1.4 M NaCl, 20 mM EDTA pH 8.0, 100 mM Tris.HCl. pH 8.0, 1% polyvinylpyrollidone). After extraction with chloroform: isoamylalcohol (24:1), 10% CTAB was added to the aqueous layer and the

chloroform:isoamylalcohol extraction repeated. . Genomic DNA was precipitated with isopropanol.

The resulting DNA was digested with restriction endonuclease *Sau*3A1 following standard procedures, extracted once with phenol:chloroform:isoamylalcohol (25:24:1) and ethanol precipitated. The digested fragments were separated on a sucrose density gradient using ultracentrifugation. Fractions containing fragments of 9-23 kb were pooled and ethanol precipitated. The resulting fragments were cloned into the lambda DASH II/*Bam*HI vector (Stratagene, La Jolla, CA) following the manufacturer's protocol and packaged using a Gigapack II Packaging Extract (Stratagene). The library was amplified once.

The library was screened with radiolabeled EST fragments isolated from a *Eucalyptus grandis* library (as described in Example 1), that showed homology to the *Eucalyptus* EF1-alpha gene. Phage lysates were prepared from positive plaques and genomic DNA was extracted.

From this genomic DNA, the 5'UTR region containing the putative promoter of the *Eucalyptus* EF1-alpha gene was obtained using the ELONGASE Amplification System (Gibco BRL). A 10 kb fragment was amplified and restriction mapped. The putative promoter region of the *Eucalyptus* elongation factor A (EF1-alpha) gene was identified on a 4kb fragment, which was subcloned into a pUC19 vector (Gibco BRL) containing an engineered *Not*I-site. The determined genomic DNA sequences of the isolated fragment containing the promoter region are provided in SEQ ID NO: 61 and 62, with the amino acid encoded by SEQ ID NO: 61 being provided in SEQ ID NO: 79. An extended sequence of the clone of SEQ ID NO: 61 is provided in SEQ ID NO: 127.

EXAMPLE 10

Isolation of Flower-Specific Promoters from *Eucalyptus grandis*

Plant polynucleotide sequences specific for flower-derived tissue were isolated from *Eucalyptus grandis* cDNA expression libraries prepared from flower tissue, essentially as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, several sequences, each containing a putative *Eucalyptus grandis* flower-specific promoter, were isolated from genomic DNA. The determined nucleotide sequences are given in SEQ ID NO: 29-33 and 59. An extended sequence of the clone of SEQ ID NO: 30-33 is provided in SEQ ID NO: 89. An extended sequence of the clone of SEQ ID NO: 29 is provided in SEQ ID NO: 90.

EXAMPLE 11

Isolation of Pollen-Specific Promoters from *Eucalyptus grandis* and *Pinus radiata*

Plant polynucleotide sequences specific for pollen were isolated from *Eucalyptus grandis* and *Pinus radiata* cDNA expression libraries prepared from pollen, essentially as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, several sequences, each containing a putative pollen-specific promoter, were isolated from genomic DNA. The determined nucleotide sequences isolated from *Pinus radiata* are given in SEQ ID NO: 49-53, with the predicted amino acid sequences encoded by SEQ ID NO: 51-53 being provided in SEQ ID NO: 73-75, respectively. An extended sequence for the clone of SEQ ID NO: 49 is provided in SEQ ID NO: 94.

EXAMPLE 12

Isolation of Bud-Specific and Meristem-Specific Promoter from *Pinus radiata*

Plant polynucleotide sequences specific for bud and meristem were isolated from *Pinus radiata* cDNA expression libraries prepared from bud and meristem, essentially as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, two sequences, one containing a putative bud-specific promoter and the other containing a putative meristem-specific promoter, were isolated from genomic DNA. The determined nucleotide sequences for these two promoters are given in SEQ ID NO: 40 and 45, respectively. The predicted amino acid sequences encoded by the DNA sequences of SEQ ID NO: 40 and 45 are provided in SEQ ID NO: 70 and 71, respectively.

EXAMPLE 13

Isolation of Promoters from *Eucalyptus grandis*

Plant polynucleotide sequences showing some homology to various known genes were isolated from *Eucalyptus grandis* cDNA expression libraries essentially as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, sequences containing the putative promoters for the following *E. grandis* genes were isolated from genomic DNA: auxin induced protein (SEQ ID NO: 26-28); carbonic anhydrase (SEQ ID NO: 36); isoflavone

reductase (SEQ ID NO: 37 and 38); pollen allergen (SEQ ID NO: 23-25); pollen coat protein (SEQ ID NO: 22), sucrose synthase (SEQ ID NO: 56-58); ubiquitin (SEQ ID NO: 34); glyceraldehyde-3-phosphate dehydrogenase (SEQ ID NO: 35 and 39); O-methyl transferase (OMT; SEQ ID NO: 60); macrophage migration inhibition factor from mammals (MIF; SEQ ID NO: 81-86); UDP glucose 6-dehydrogenase (SEQ ID NO: 103); laccase 1 (SEQ ID NO: 105, 106 and 116); arabinogalactan-like 1 (SEQ ID NO: 107); arabinogalactan-like 2 (SEQ ID NO: 108, 109); a hypothetical protein (SEQ ID NO: 104); constans (SEQ ID NO: 118); Flowering Promoting Factor 1 (FPF1; SEQ ID NO: 119); transcription factor DREB-1 (SEQ ID NO: 121); salt tolerance protein (SE QID NO: 123); xylem-specific histidine kinase-like (SEQ ID NO: 125) and root specific (SEQ ID NO: 126). The amino acid sequences encoded by the DNA sequences of SEQ ID NO: 22, 25, 26, 28, 34, 35, 36, 56, 57, 60, 86 and 124 are provided in SEQ ID NO: 63, 64, 65, 66, 67, 68, 69, 76, 77, 78, 87 and 130, respectively. Extended cDNA sequences for the clones of SEQ ID NO: 58, 35, 60, 103, 106 and 107 are provided in SEQ ID NO: 91, 93, 113 and 115-117, respectively.

EXAMPLE 14

Isolation of Promoters from *Pinus radiata*

Plant polynucleotide sequences showing some homology to various known genes were isolated from *Pinus radiata* cDNA expression libraries essentially as described in Example 1. Using the "Genome Walker" protocol described above and gene specific primers designed from these plant polynucleotide sequences, sequences containing the putative promoters for the following *Pinus radiata* genes were isolated from genomic DNA: senescence-like protein (SEQ ID NO: 46-48); nodulin homolog pollen specific (SEQ ID NO: 54 and 55); chalcone synthase (SEQ ID NO: 88); PrMALE1 (SEQ ID NO: 95, 96); UDP glucose glycosyltransferase (SEQ ID NO: 97); elogation factor 1 alpha (SEQ ID NO: 98, 99); S-adenosylmethionine synthase (SEQ ID NO: 100-102); *Pinus radiata* lipid transfer protein 2 (PrLTP2; SEQ ID NO: 112); *Pinus radiata* agamous protein (SEQ ID NO: 120); Drought Induced DI-19 (SEQ ID NO: 122) and low temperature induced protein LTI (SEQ ID NO 124). The amino acid sequences encoded by the polynucleotide sequences of SEQ ID NOS: 46 and 124 are provided in SEQ ID NOS: 72 and 130. An extended cDNA sequence for the clone of SEQ ID NO: 97 is provided in SEQ ID NO: 114.

EXAMPLE 15

Polynucleotide and Amino Acid Analysis

The determined cDNA sequences described above were compared to and aligned with known sequences in the EMBL database (as updated to October 2000). Specifically, the polynucleotides identified in SEQ ID NOS: 22-62 and 88-120 were compared to polynucleotides in the EMBL database using the BLASTN algorithm Version 2.0.6 [Sept-16-1998] and the polynucleotides identified in SEQ ID NOS: 121-127 were compared to polynucleotides in the EMBL database using the BLASTN algorithm Version 2.0.11 [Jan-20-2000] set to the following running parameters: Unix running command: blastall –p blastn –d embldb –e 10 –G0 –E0 –r1 –v30 –b30 –i queryseq –o results. Multiple alignments of redundant sequences were used to build up reliable consensus sequences. Based on similarity to known sequences from other plant or non-plant species, the isolated polynucleotides of the present invention identified as SEQ ID NOS: 22-62 and 88-127 were putatively identified as having the functions shown in Table 1, above.

The cDNA sequences of SEQ ID NO: 1-22, 23, 25-42, 45-49, 57-59, 62, 88-99, 101-112 and 114-127 were determined to have less than 40% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The cDNA sequences of SEQ ID NO: 56 and 113 were determined to have less than 60% identity to sequences in the EMBL database using BLASTN, as described above. The cDNA sequences of SEQ ID NO: 43, 52, 60 and 61 were determined to have less than 75% identity to sequences in the EMBL database using BLASTN, as described above. The cDNA sequences of SEQ ID NO: 24, 51 and 100 were determined to have less than 90% identity to sequences in the EMBL database using BLASTN, as described above.

EXAMPLE 16

Modification of a Reporter Gene under Control of the Superubiquitin Promoter

Six independent *Arabidopsis thaliana* transgenic lines were transformed with *Pinus radiata* superubiquitin promoter constructs to demonstrate the relative expression of a GUS reporter gene under control of different superubiquitin promoter constructs. The reporter constructs in the plasmid pBI-101 contained the GUS (β-D-glucuronidase) reporter gene in frame with the superubiquitin promoter with the intron (SEQ ID NO: 2), the superubiquitin

promoter without the intron (SEQ ID NO: 3), and the CaMV 35S promoter. A reporter gene construct without a promoter sequence was used as control.

Groups of six *Arabidopsis thaliana* plants were transformed with the reporter constructs described above, using *Agrobacterium tumefaciens* transformation protocols. *A. tumefaciens* was transformed with 100 ng of the plasmid DNA according to standard techniques, as described, for example, by Bevan (*Nucleic Acids Res.* 12:8711-8721, 1984). Fresh plant material was collected from each plant, protein extracted from the whole plant, and the protein concentration determined (Bradford, *Anal. Biochem.* 72:248-254, 1976). The protein samples were diluted with carrier bovine serum albumin to 100 ng protein to maintain readings on the fluorimeter in the linear part of the standard curve using 4-methyl-umbelliferone (MU). GUS activity was quantified by fluorimetric analysis, using a Victor^2 1420 multi-label counter (Wallac, Turku, Finland) as described by Jefferson (*Plant Mol. Biol. Rep.* 5:387-405, 1987). As shown in Fig. 1, the construct containing the superubiquitin promoter without the intron showed seven times more GUS activity than the CaMV 35S promoter and the construct containing the superubiquitin promoter with the intron showed sixty two times more GUS activity than the CaMV 35S promoter. No activity was detected for the promoter-less control construct.

EXAMPLE 17

Determination of the Activity of Superubiquitin Promoter Constructs in Tobacco Plant Protoplasts

Isolation of protoplasts

Protoplasts were isolated from sterile tobacco (*Nicotiana tabacum*) leaf tissue and transformed with superubiquitin promoter constructs. Mesophyll protoplasts were prepared according to the method of Bilang *et al.*, *Plant Molecular Biology Manual* A1:1-16, 1994. A number of fully expanded leaves were removed from sterile wild type tobacco plants, sliced perpendicular to the midrib and submerged in a digestion enzyme solution containing 1.2% cellulase and 0.4% pectinase (Sigma, St. Louis MO). The leaves were left to incubate in the dark without agitation at 26°C for approximately 18 hours. The leaf strips were then gently agitated for 30 min to release the protoplasts. Protoplasts were further purified by filtration through 100 µm nylon mesh. One ml of W5 solution (154 mM $MgCl_2$, 125 mM $CaCl_2$, 5 mM KCl, 5 mM glucose, pH 5.8 - 6) was carefully layered on top of the filtrate and

centrifuged at 80 x g for 10 min. The live protoplast layer was removed with a wide bore pipette, washed twice with 10 ml W5 solution using centrifugation at 70 x g for 5 min, with final resuspension in 5 ml W5 solution. Protoplasts were counted in a hemocytometer and viability was determined under the microscope after staining with 5 mg/ml fluoroscein diacetate (FDA) in 100% acetone.

Transformation with promoter constructs

The isolated protoplasts were transformed with plasmid DNA using a polyethylene glycol protocol. After centrifugation of the purified protoplasts at 70 x g for 5 min, they were resuspended in MMM solution (15 mM $MgCl_2$, 0.1% w/v 2[N-morpholino]ethanesulfonic acid (MES), 0.5 M mannitol pH 5.8) to a density of 2 x 10^6 protoplasts/ml. Aliquots containing 5 x 10^5 protoplasts/ml in 250 µl were distributed to 15 ml tubes and mixed with 20 µg plasmid DNA. 250 µl polyethylene glycol-4000 (40%) was gently added and incubated for 5 minutes at room temperature. Ten ml W5 solution was slowly added, the protoplasts centrifuged at 70 x g for 5 min and finally resuspended in 2 ml K3 medium (Bilang *et al.*, *Plant Molecular Biology Manual* A1:1-16, 1994). The transformed protoplasts were incubated in the dark at 26°C for 24 hours before protein was extracted for reporter enzyme assays using 4-methyl-umbelliferyl-glucuronide (MUG).

Protein was extracted from the protoplasts using the following protocol. Transformed protoplast suspensions were centrifuged at 70 x g for 10 min, resuspended in 50 µl extraction buffer (Jefferson, *Plant Mol. Biol. Rep.* 5:387-405, 1987) and vigorously mixed using a vortex. The homogenate was cleared by centrifugation at 4,300 rpm for 5 min, the supernatant removed and used for protein assays (Bradford, *Anal. Biochem.* 72:248-254, 1976).

The results shown in Fig. 2 demonstrate the promoter activity of deletion constructs of the superubiquitin promoter without the intron (SEQ ID NO: 3) and the superubiquitin promoter with the intron (SEQ ID NO: 2) in tobacco plant protoplasts transformed as described above. The deletion constructs were made in plasmid pBI-101 that contained the GUS reporter gene, using Endonuclease III (Gibco BRL, Gaithersburg, MD) according to the manufacturer's protocols. The deletion constructs contained 1,103; 753; 573; 446; 368 and 195 bp of superubiquitin promoter sequence, respectively, upstream of the TATA sequence (bp numbers 1,104-1,110 of SEQ ID NO: 2). A control construct containing no sequence upstream of the TATA sequence was also made. These results show that the construct

containing the entire superubiquitin promoter with the intron had the highest MU activity in the protoplasts.

In Fig 3, the tobacco protoplasts were transformed with four different promoter constructs in plasmid pBI-101 containing the GUS reporter gene. These included the superubiquitin promoter without the intron (SEQ ID NO: 3), an elongation factor 1α promoter (SEQ ID NO: 99) and a 5-adenosylmethionine synthetase promoter (SEQ ID NO: 100). A promoterless control was included in the experiment, and is referred to in Fig. 3 as pBI-101.

EXAMPLE 18

Determination of the Activity of *P. radiata* Pollen-specific Promoter and *E. grandis* Pollen Specific Promoter Constructs in transformed *Arabidopsis thaliana* cv Columbia

Arabidopsis thaliana transgenic lines were transformed with *A. tumefaciens* containing constructs of the *P. radiata* pollen specific promoter (SEQ ID NO: 94) and *E. grandis* pollen specific promoter (SEQ ID NO: 22) to demonstrate the relative expression of a GUS reporter gene under control of these promoter constructs. The promoter sequences were cloned into plasmid pBI-101 containing a GUS reporter gene.

Agrobacterium tumefaciens transformation

Agrobacterium tumefaciens strain GV3101 was transformed with these constructs using electroporation. Electrocompetent *A. tumefaciens* cells were prepared according to the method of Walkerpeach and Velten, *Plant Mol. Biol. Man.* B1:1-19, 1994. Construct DNA (4 ng) was added to 40 µl competent *A. tumefaciens* GV3101 cells and electroporation was done using a BTX Electro Cell Manipulator 600 at the following settings: Mode: T 2.5kV Resistance high voltage (HV), Set Capacitance: C (not used in HV mode), Set Resistance: R R5 (129 Ohm), Set charging voltage: S 1.44kV, Desired field strength: 14.4kV/cm and Desired pulse strength: t 5.0 msec. 400 µl YEP liquid media (20g/l yeast, 20 g/l peptone and 10 g/l sodium chloride) was added to the cuvette and left to recover for one hour at room temperature. Transformed bacteria in YEP medium were spread out on solid YEP medium containing 50 mg/l kanamycin and 50 mg/l rifampicin and incubated at 29°C for two days to allow colony growth.

Confirmation of transformation of constructs into *A. tumefaciens*

To confirm that the constructs have been transformed into *A. tumefaciens*, DNA from the *A. tumefaciens* colonies from the YEP plates were isolated using standard protocols and amplified using the polymerase chain reaction (PCR) with primers designed from the pBI-101 vector sequence. The primer sequences are given in SEQ ID NOS: 128 and 129. PCR reactions were set up following standard protocols and 30 PCR cycles were done with extension temperature of 72°C.

Transformation of *A. thaliana* with transformed *A. tumefaciens*

The optical density of the *A. tumefaciens* bacterial culture was adjusted to 0.7 with infiltration medium (5% sucrose, 0.05% Silwett L-77 surfactant). *A. thaliana* cv. Columbia plants (6 punnets per construct and 10-12 plants per punnet) were pruned by removing secondary bolts. Pruned *A. thaliana* plants in punnets were dipped into infiltration solution and moved back and forth for 5 seconds. Punnets were put on their side to allow excess infiltration medium to drain covered with a top tray and wrapped in plastic wrap to maintain humidity. Plants were placed in a growth room at ambient conditions for 24 hours. After this period, the top tray and plastic wrap were removed and plants were set upright until siliques formed.

Seeds were harvested and sterilized with a 5% sodium hypochlorite solution to destroy any residual *A. tumefaciens* bacteria and fungal contamination.

Under sterile conditions, 100 µl seeds from the transformed *A. thaliana* plants were placed into an Eppendorf tube. One ml sterile water was added and the seeds left to imbibe the water for no longer than an hour. The water was remove by centrifugation, 1 ml 70% ethanol added to the seeds and gently mixed. This step was not allowed to last longer than one minute. The ethanol was removed by centrifugation, 1 ml 5% sodium hypochlorite solution was added to the seeds and gently mixed for up to 5 min. The sodium hypochlorite solution was removed by centrifugation and the seeds washed with sterile water for 1 min. The washing step was repeated three more times with centrifugation. Seeds were finally resuspended in sterile water. 500 µl of seeds in solution were pipetted onto half-strength Murashige and Skoog medium (MS; Gibco BRL) agar plates containing 50 mg/l kanamycin and 250 mg/l timentin and spread evenly with a flamed wire-loop. The Petri dishes were placed in a refrigerator for 3 days to allow the seeds to stratify. Thereafter the plates were placed in growth room and grown under lights at 22°C with a 14 hour photoperiod until

germination. Putative transformant seedlings were selected as those growing on the antibiotic-containing medium, with large, healthy-looking dark green leaves and a strong root system. These transgenic plants were removed and placed into soil culture at 22°C with a 12 hour photoperiod.

Staining of plant tissues

Tissue were taken from the flower, leaf, stem and root of *A. thaliana* transformed with constructs of *P. radiata* unknown pollen specific promoter and *E. grandis* pollen specific promoter and stained histochemically to determine the expression of the GUS gene under control of the pollen specific promoters. The GUS staining protocol is described by Campisi *et al.*, *Plant J.* 17:699-707, 1999.

A. thaliana flower, leaf, stem and root tissue were immersed in staining solution (50 mM $NaPO_4$ pH 7.2; 0.5% Triton X-100; 1 mM X Glucuronide sodium salt (Gibco BRL)) for immunochemical staining. Vacuum was applied twice for 5 min to infiltrate the tissue with the staining solution. The tissue was left in the staining solution for 2 days (with agitation) at 37° for color development and then destained in 70% ethanol for 24 hours at 37°C (with agitation). The tissues were examined for blue GUS staining using a light microscope. GUS expression was observed only in the flower buds of plants transformed with the *P. radiata* pollen specific promoter construct, and not in the leaf, stem or root tissue. With the *E. grandis* pollen specific promoter construct, Gus expression was observed in the floral buds as well as in the hydathodes of the leaves. No expression was observed in the stem or root tissues.

To determine in which cell layers the GUS gene was expressed, flower buds were fixed for thin sectioning. The flower buds were fixed with formaldehyde acetic acid (FAA) in an Eppendorf tube and vacuum was applied twice for 15 min. After incubation for 2 hours at room temperature, vacuum was again applied for 15 min and the tissue left overnight at 4°C. The tissues were then dehydrated using a series of ethanol and then passed into a xylene series. Paraffin wax (Sigma) was added slowly and the tissues left for 72 hours with wax changes every 12 hours. Sections of 8 to 10 μm thickness were prepared using a microtome.

The thin sections illustrated that GUS expression was restricted to the tapetum cell layer in the anther of the floral bud of *A. thaliana* transformed with the *P. radiata* construct (SEQ ID NO: 49). No staining was observed in other tissues from the floral bud. GUS expression was confined to the pollen grains within the flower bud of *A. thaliana*

transformed with the *E. grandis* pollen specific promoter construct, with low levels of GUS expression in the fibrous and connective tissue of the anther. No GUS expression was observed in other organs of the floral bud.

EXAMPLE 19

Determination of the Activity of an *E. grandis* EF1 alpha Promoter Deletion Construct in transformed *Arabidopsis thaliana* cv Columbia

Protoplasts from *Nicotiana tabacum* Bright Yellow 2 (BY-2) cell suspension were transformed with a deletion construct of the *E. grandis* EF1-alpha promoter to determine GUS expression. Base pairs 2,174 to 3,720 of SEQ ID NO: 127 were cloned into expression vector pART9, containing the reporter gene GUS and an OCS termination sequence.

Preparation of protoplasts

Sterile *Nicotiana tabacum* Bright Yellow-2 (BY-2) suspension cultures were prepared as described in Example 17. After incubation for 3 to 5 days, 3 g of the *N. tabacum* BY-2 cell suspension were suspended in an enzyme solution containing 1% cellulase, 0.3% pectinase and 0.5% driselase in 0.4 M mannitol. These were left to digest in the dark, with agitation at 26° C, for 3-4 hours. Protoplasts were purified by filtration through a 63 µm nylon mesh. Protoplasts were centrifuged at 80x g for 5 min, washed twice with 10 ml FMS medium (Fukuda, Murashige and Skoog medium; Hasezawa & Syono, *Plant Cell Physiol.* 24:127-132, 1983) and finally resuspended in 5 ml FMS medium. Protoplasts were counted in a hemocytometer and viability determined by staining with 5 mg/ml FDA (fluorescein deacetate; Sigma St Louis MI) in 100% acetone by viewing under the fluorescent microscope.

Transformation of Protoplasts

Protoplasts were transformed according to the protocol described by Morgan and Ow (In: Methods in Plant Molecular Biology: a laboratory course manual, pp. 1-16. P. Maliga, D.Klessig, A.R. Cashmore, W. Gruissem, and J.E.Varner, eds. Cold Spring Harbor Laboratory, CSHP, NY). Briefly, the protocol is as follows. Following the counting step, protoplasts were centrifuged at 80x g for 5 min and resuspended in 1x MaMg solution (0.4 M manniotol, 15 mM $MgCl_2.6H_2O$, 0.1% 2-(*N*-Morpholino)ethane sulfonic acid (MES)) to a density of $5x10^6$ protoplasts/ml. Aliquots of 100 µl (0.5×10^5 protoplasts) were distributed to

15 ml tubes and washed with 5 ml 1x MaMg (200g, 5 min). Pelleted protoplasts were resuspended in 500ul 1x MaMg solution, and heat shocked by placing at 45°C for 5 minutes. After incubation at room temperature 5-10 minutes, the transforming DNA was added (10-20 μg DNA + 10 μg carrier DNA). To this, 500 μl 40% PEG-3500 was gently added and incubated for 25 minutes at room temperature. 5ml W5 (154 mM NaCl, 125 mM $CaCl_2.2H_2O$, 5 mM KCl, 5 mM Glucose) solution was slowly added stepwise followed by centrifugation at 200x g for 5 min. Pelleted protoplasts were resuspended in 1ml K3AM medium at approximately 0.5 x 10^5 protoplasts/ml. Samples were transferred to 6-well plates and incubated in the dark at 26°C for 48 hours.

To extract protein, protoplasts were centrifuged at 200x g for 5 min in a microfuge, resuspended in 100 μl GUS extraction buffer (50 mM $NaPO_4$ pH 7.2, 10 mM EDTA pH 8, 0.01% Sarcosyl, 0.1% Triton X-100) containing β-mercaptoethanol (Jefferson et al., *Plant Mol. Biol. Rep.* 5:387-405, 1987) and vortexed for 1 min. The homogenate was cleared by centrifugation at 5,000 rpm for 5 minutes. The supernatant containing the protein was transferred to a fresh tube and stored at -80°C. The protein concentrations were determined by BioRad protein assay kit (BioRad, Hercules, CA) following the manufacturer's protocols. Protein extracts were diluted 1/10 with extraction buffer.

Determination of GUS expression

GUS expression in the protoplast extracts was determined using a MUG (4-methyl umbelliferyl β-D-glucuronide) assay. Protein samples, containing 1 μg protein made up to a total volume of 45 μl with extraction buffer, were aliquoted onto a microtitre plate and incubated at 37°C. To each sample, 5 μl of 10 mM MUG was added so that the final concentration of MUG was 1 mM. The plate was incubated at 37°C for 30 min and terminated by adding 150 μl stop solution (0.2 M Na_2CO_3, pH 11.20), still keeping the plates at 37°C. Plates were read in a Victor^2 1420 Multilabel counter with excitation set at 365 nm and emission at 455 nm. The concentration of 4-methyl-umbelliferone (MU) was calculated against a standard curve and the GUS expression calculated.

In Fig. 4, increased expression of the GUS reporter gene in *N. tabacum* BY-2 protoplasts transformed with an *E. grandis* EF1 alpha deletion construct was seen compared to the control plasmid without an insert.

EXAMPLE 20

Determination of the Effect of the 3'UTR Super-ubiquitin (SU) Sequences on Gene Expression in *Arabidopsis thaliana* cv Columbia

In the polynucleotide sequences given in SEQ. ID NO: 1 encoding *P. radiata* superubiquitin (SU) promoter and gene sequences, an 3' untranslated region (UTR) was identified (nucleotides 1,754 to 3,083). To determine the effect of this region on the expression of genes, 250 bp of the 3' UTR (nucleotides 2,755 to 3,073 from SEQ ID NO: 1) was cloned in the sense and antisense orientation into plasmid pBI-121 containing the GUS gene under control of the 35S CaMV promoter and plasmid pBI-101 containing the GUS gene under control of the *P. radiata* SU promoter (including the intron) given in SEQ ID NO: 2. For controls, constructs were made that contained the SU promoter without an intron (SEQ ID NO: 3) and without the SU 3' UTR sequence, the SU promoter with an intron (SEQ ID NO: 2) and without the SU 3' UTR sequence as well as a construct containing the 35S CaMV promoter but not the SU 3' UTR sequence.

A. thaliana cv Columbia were transformed with these constructs using the floral dip protocol described in Example 18.

Determining the level of gene expression using a MUG assay.

Six *A. thaliana* plants were harvested by trimming off the dried tissue and then harvesting the rest of the plant, including the roots. The roots were rinsed in tap water and the samples immersed in liquid nitrogen before storing at -80°C. Six plants from each construct were ground under liquid nitrogen and approximately 100 mg transferred to a microfuge tube. Five samples from each control were included in the assay. Extraction buffer (50 mM $NaPO_4$ pH 7.2, 10 mM EDTA pH 8, 0.01% Sarcosyl, 0.1% Triton X-100) was prepared. To 32 ml of extraction buffer, 8 ml methanol and 28 μl β-mercaptoethanol was added. Of this buffer, 200 μl was added to each sample, vortexed and stored on ice. Samples were spun at 4°C at 15, 000 rpm for 15 min. The supernatant was transferred to a fresh tube and diluted with 800 μl of extraction buffer. Protein concentration was determined using the BioRad Protein Assay Kit.

The expression of GUS by the four constructs was determined using a MUG assay, as follows. To 28 ml extraction buffer (as described in Example 18), 8 ml methanol, 56 μl β-mercaptoethanol and 4 ml of 10 mg/ml bovine serum albumin (BSA) were added. To

microtitre plate wells, 100 and 10 ng of protein from each construct was added as well as 25 μl extraction buffer containing BSA and 5 μl 10 mM MUG. The plate was covered in foil and incubated at 37°C for exactly 20 minutes. The reaction was terminated by adding 150 μl 0.2 M Na_2CO_3 pH 11.2. Plates were read with a Victor^2 1420 Multilabel counter with excitation set at 365 nm and emission at 455 nm. GUS expression levels were determined against a MU standard curve.

In Fig. 5, construct SR34 containing the SU 3'UTR in the sense orientation enhanced the expression of the SU without intron promoter almost to the level of the SU promoter with the intron. In constructs SR33 and SR35 containing the 3'UTR in the antisense orientation, promoter activity was reduced to basal levels.

Claims:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:
   (a) sequences recited in SEQ ID NO: 2-14, 20, 22-33, 35-43, 45-49, 51, 52, 56-62 and 88-127;
   (b) complements of the sequence recited in SEQ ID NO: 2-14, 20, 22-33, 35-43, 45-49, 51, 52, 56-62 and 88-127;
   (c) reverse complements of the sequence recited in SEQ ID NO: 2-14, 20, 22-33, 35-43, 45-49, 51, 52, 56-62 and 88-127;
   (d) reverse sequences of the sequences recited in SEQ ID NO: 2-14, 20, 22-33, 35-43, 45-49, 51, 52, 56-62 and 88-127;
   (e) sequences having at least 40% identical nucleotides to a sequence provided in SEQ ID NO: 2-14, 20, 22-23, 25-33, 35-42, 45-49, 57-59, 62, 88-99, 101-112 and 114-127 as determined using the computer algorithm BLASTN;
   (f) sequences having at least 60% identical nucleotides to a sequence provided in SEQ ID NO: 2-14, 20, 22-23, 25-33, 35-42, 45-49, 56-59, 62, 88-99, 101-112 and 114-127 as determined using the computer algorithm BLASTN;
   (g) sequences having at least 75% identical nucleotides to a sequence provided in SEQ ID NO: 2-14, 20, 22-23, 25-33, 35-49, 52, 56-61, 62, 88-99, 101-112 and 114-127 as determined using the computer algorithm BLASTN; and
   (h) sequences having at least 90% identical nucleotides to a sequence provided in SEQ ID NO: 2-14, 20, 22-33, 35-49, 51, 52, 56-61, 62, 88-112 and 114-127 as determined using the computer algorithm BLASTN.
2. An isolated polynucleotide comprising a sequence selected from the group consisting of:
   (a) sequences recited in SEQ ID NO: 1 and 34;
   (b) complements of sequences recited in SEQ ID NO: 1 and 34;
   (c) reverse complements of sequences recited in SEQ ID NO: 1 and 34;
   (d) reverse sequences of sequences recited in SEQ ID NO: 1 and 34;
   (e) sequences having at least 40% identical nucleotides to sequences recited in SEQ ID NO: 1 and 34 as determined using the computer algorithm BLASTN;
   (f) sequences having at least 60% identical nucleotides to sequences recited in SEQ ID NO: 1 and 34 as determined using the computer algorithm BLASTN;

(g) sequences having at least 75% identical nucleotides to sequences recited in SEQ ID NO: 1 and 34 as determined using the computer algorithm BLASTN; and

(h) sequences having at least 90% identical nucleotides to sequences recited in SEQ ID NO: 1 and 34 as determined using the computer algorithm BLASTN.

3. An isolated polypeptide encoded by a polynucleotide selected from the group consisting of:

(a) sequences recited in SEQ ID NO: 1, 22, 25, 26, 28, 34, 35, 36, 40, 45, 46, 51-53, 56, 57, 60, 61, 86 and 124;

(b) complements of the sequences of SEQ ID NO: 1, 22, 25, 26, 28, 34, 35, 36, 40, 45, 46, 51-53, 56, 57, 60, 61, 86 and 124;

(c) reverse complements of a sequence of SEQ ID NO: 1, 22, 25, 26, 28, 34, 35, 36, 40, 45, 46, 51-53, 56, 57, 60, 61, 86 and 124;

(d) reverse sequences of a sequence of SEQ ID NO: 1, 22, 25, 26, 28, 34, 35, 36, 40, 45, 46, 51-53, 56, 57, 60, 61, 86 and 124;

(e) sequences having at least 40% identical nucleotides to a sequence provided in SEQ ID NO: 1, 22, 25, 26, 28, 34, 35, 36, 40, 45, 46, 51-53, 56, 57, 60, 61, 86 and 124;

(f) sequences having at least 60% identical nucleotides to a sequence provided in SEQ ID NO: 1, 22, 25, 26, 28, 34, 35, 36, 40, 45, 46, 51-53, 56, 57, 60, 61, 86 and 124;

(g) sequences having at least 75% identical nucleotides to a sequence provided in SEQ ID NO: 1, 22, 25, 26, 28, 34, 35, 36, 40, 45, 46, 51-53, 56, 57, 60, 61, 86 and 124; and

(h) sequences having at least 90% identical nucleotides to a sequence provided in SEQ ID NO: 1, 22, 25, 26, 28, 34, 35, 36, 40, 45, 46, 51-53, 56, 57, 60, 61, 86 and 124.

4. The isolated polypeptide of claim 3, wherein the polypeptide comprises a sequence selected from the group consisting of SEQ ID NO: 63-80, 87 and 130.

5. A genetic construct comprising a polynucleotide according to any one of claims 1 and 2.

6. A genetic construct comprising, in the 5'-3' direction:

(a) a promoter sequence,

(b) a DNA sequence of interest; and

(c) a gene termination sequence,

wherein the promoter sequence comprises an isolated polynucleotide according to claim 1.

7. The genetic construct of claim 6, wherein the DNA sequence of interest comprises an open reading frame encoding a polypeptide of interest.

8. The genetic construct of claim 6, wherein the DNA sequence of interest comprises a non-coding region of a gene encoding a polypeptide of interest.

9. A transgenic cell comprising a genetic construct of any one of claims 5-8.

10. An organism comprising a transgenic cell according to claim 9.

11. A plant comprising a transgenic cell according to claim 9, or a part or propagule or progeny thereof.

12. A method for modifying gene expression in a target organism comprising stably incorporating into the genome of the organism a genetic construct according to any one of claims 5-8.

13. The method of claim 12 wherein the organism is a plant.

14. A method for producing a plant having modified gene expression comprising:

(a) transforming a plant cell with a genetic construct to provide a transgenic cell, wherein the genetic construct comprises: (i) a promoter sequence comprising a sequence of SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127; (ii) a DNA sequence of interest; and (c) a gene termination sequence; and

(b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

15. A method for modifying a phenotype of a target organism, comprising stably incorporating into the genome of the target organism a genetic construct comprising:

(a) a promoter sequence comprising a sequence of SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127;

(b) a DNA sequence of interest; and

(c) a gene termination sequence.

16. The method of claim 15, wherein the target organism is a plant.

17. A method for identifying a gene responsible for a desired function or phenotype, comprising:

(a) transforming a plant cell with a genetic construct comprising a promoter sequence operably linked to a gene to be tested, the promoter sequence comprising a sequence of SEQ ID NO: 1-14, 20, 22-62, 81-86 and 88-127;

(b) cultivating the plant cell under conditions conducive to regeneration and mature plant growth to provide a transgenic plant; and

(c) comparing the phenotype of the transgenic plant with the phenotype of non-transformed plants.

18. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) a sequence recited in SEQ ID NO: 21;

(b) complements of a sequence recited in SEQ ID NO: 21;

(c) reverse complements of a sequence recited in SEQ ID NO: 21;

(d) reverse sequences of a sequence recited in SEQ ID NO: 21;

(e) sequences having at least 40% identical nucleotides to a sequence recited in SEQ ID NO: 21 as determined using the computer algorithm BLASTN;

(f) sequences having at least 60% identical nucleotides to a sequence recited in SEQ ID NO: 21 as determined using the computer algorithm BLASTN;

(g) sequences having at least 75% identical nucleotides to a sequence recited in SEQ ID NO: 21 as determined using the computer algorithm BLASTN; and

(h) sequences having at least 90% identical nucleotides to a sequence recited in SEQ ID NO: 21 as determined using the computer algorithm BLASTN.

19. A genetic construct comprising a polynucleotide according to claim 18.

20. A transgenic cell comprising a genetic construct according to claim 19.

21. A method for modifying gene expression in a target organism comprising stably incorporating into the genome of the organism a genetic construct according to claim 19.

22. A method for modifying expression of a polynucleotide that comprises the sequence of SEQ ID NO: 21, the method comprising removing the sequence of SEQ ID NO: 21 from the polynucleotide.

23. A polynucleotide comprising a sequence selected from the group consisting of SEQ ID NO: 2-14, 20, 22-33, 35-43, 45-49, 51, 52, 56-62 and 88-127 operably linked to a heterologous polynucleotide.

24. The polynucleotide of claim 23, wherein the heterologous polynucleotide comprises an open reading frame.

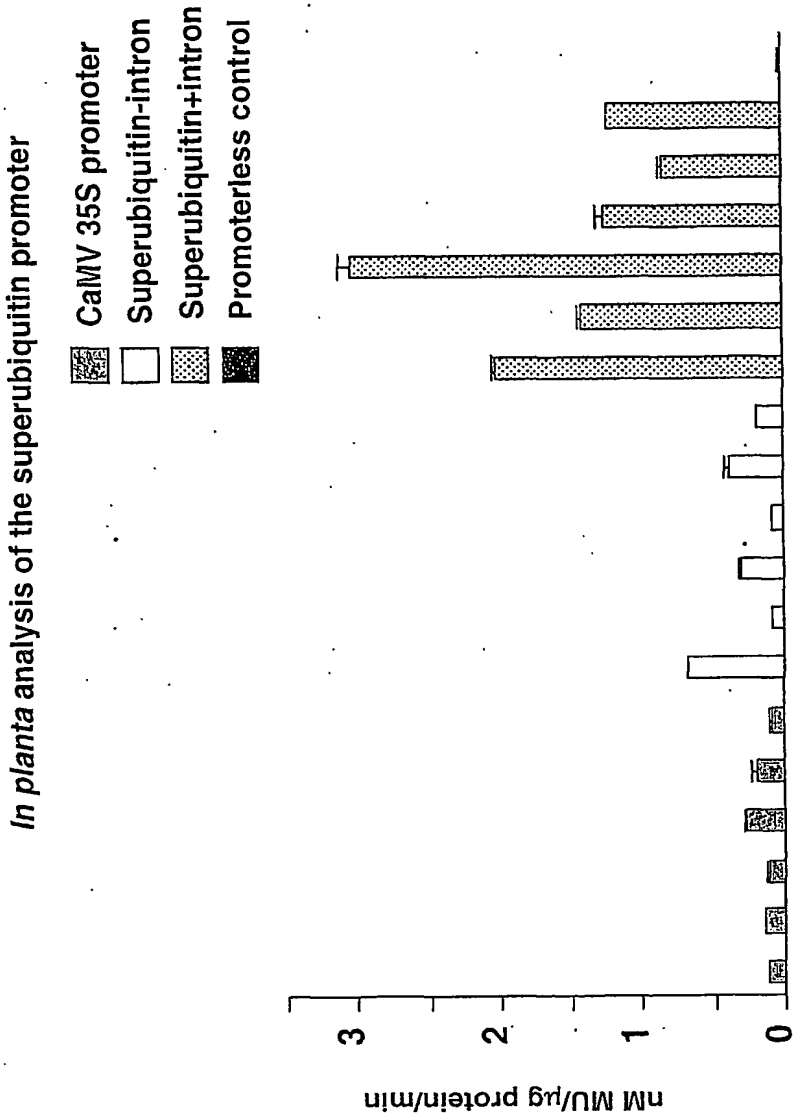
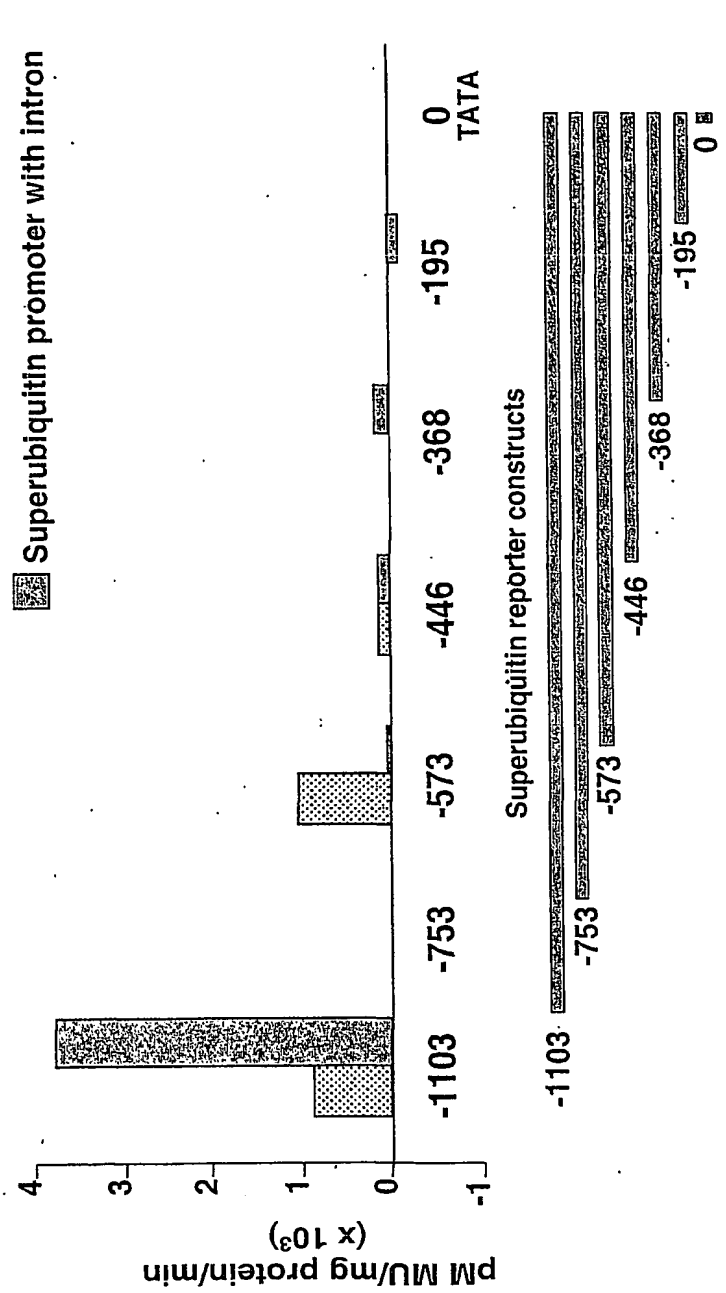

In planta analysis of the superubiquitin promoter
CaMV 35S promoter
Superubiquitin-intron
Superubiquitin+intron
Promoterless control
nM MU/µg protein/min
0
1
2
3
Individual plants

Figure 1

Figure 2

In vitro analysis of the superubiquitin promoter using deletion constructs



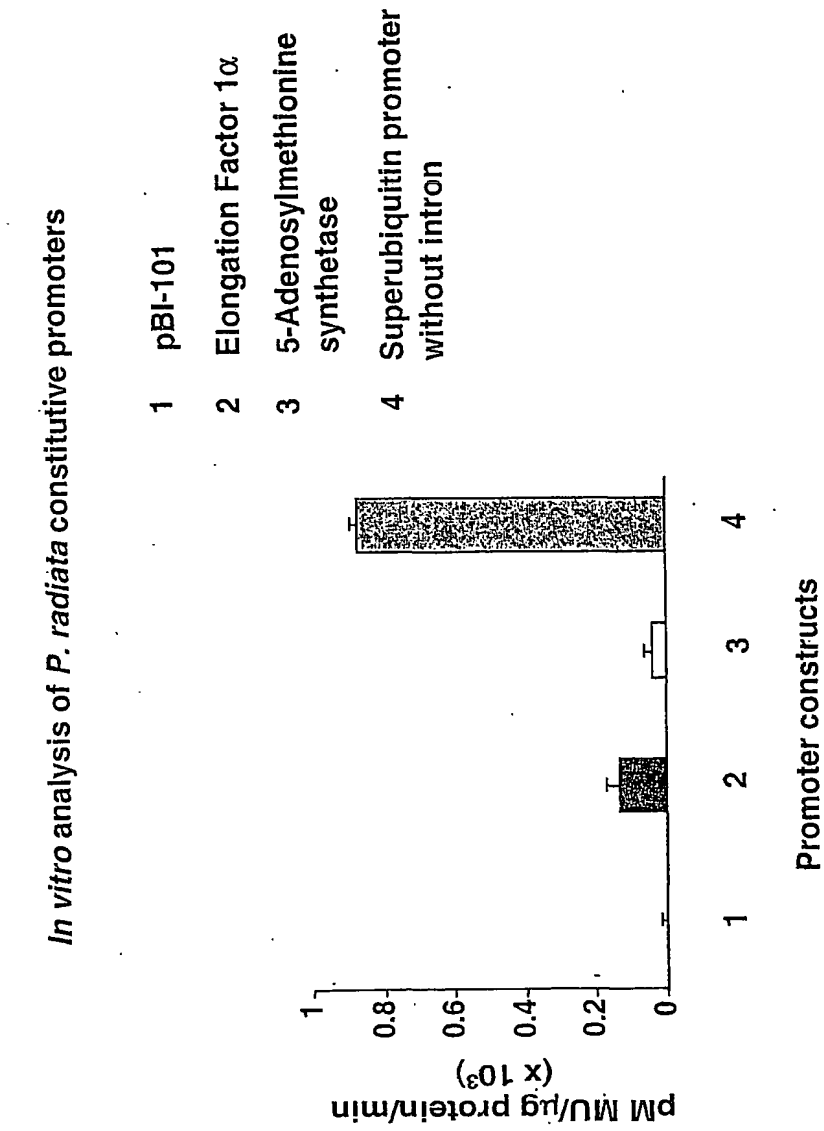
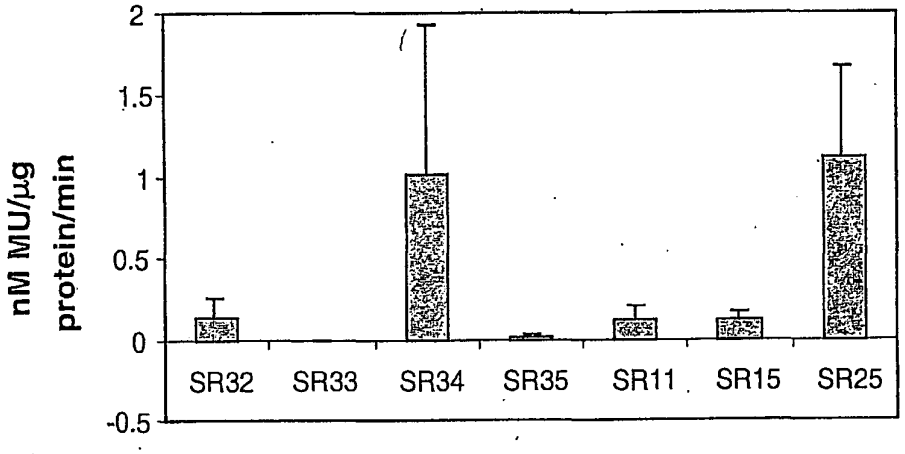

In vitro analysis of P. radiata constitutive promoters
1 pBI-101
2 Elongation Factor 1α
3 5-Adenosylmethionine synthetase
4 Superubiquitin promoter without intron
pM MU/μg protein/min (x 10³)
0
0.2
0.4
0.6
0.8
1
1 2 3 4
Promoter constructs

Figure 3

Determination of GUS expression levels in *A. thaliana* cv Columbia by constructs containing Super-ubiquitin (SU) 3' UTR sequence in sense and antisense orientation



SR32 35S CaMV promoter with sense 3' UTR

SR33 35S CaMV promoter with antisense 3' UTR

SR34 *P. radiata* SU promoter with sense 3' UTR

SR35 *P. radiata* SU promoter with antisense 3'UTR

SR11 Superubiquitin promoter without intron

SR15 35S CaMV promoter

SR25 Superubiquitin promoter with intron

Figure 4

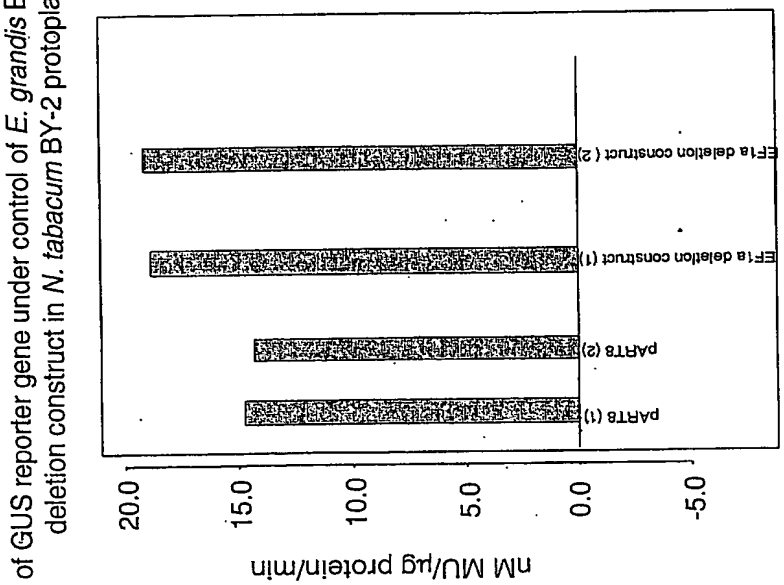

Expression of GUS reporter gene under control of E. grandis EF1 alpha promoter
deletion construct in N. tabacum BY-2 protoplasts
nM MU/µg protein/min
20.0
15.0
10.0
5.0
0.0
-5.0
pART8 (1)
pART8 (2)
EF1a deletion construct (1)
EF1a deletion construct (2)
Construct

Figure 5

SEQUENCE LISTING

<110> Perera, Ranjan
Rice, Stephen
Eagleton, Clare
Lasham, Annette

<120> Compositions and Methods for the Modification of Gene Expression

<130> 11000.1036c3PCT

<150> U.S. No. 09/598,401
<151> 2000-06-20

<150> U.S. No. 09/724,624
<151> 2000-11-28

<160> 130

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3083
<212> DNA
<213> Pinus radiata

<220>
<221> 5'UTR
<222> (1)...(2064)

<221> intron
<222> (1196)...(2033)

<221> CDS
<222> (2065)...(2751)

<221> 3'UTR
<222> (2755)...(3083)

<400> 1
aaaacccctc acaaatacat aaaaaaaatt ctttatttaa ttatcaaact ctccactacc 60
tttcccacca accgttacaa tcctgaatgt tggaaaaaac taactacatt gatataaaaa 120
aactacatta cttcctaaat catatcaaaa ttgtataaat atatccactc aaaggagtct 180
agaagatcca cttggacaaa ttgcccatag ttggaaagat gttcaccaag tcaacaagat 240
ttatcaatgg aaaaatccat ctaccaaact tactttcaag aaaatccaag gattatagag 300
taaaaaatct atgtattatt aagtcaaaaa gaaaaccaaa gtgaacaaat attgatgtac 360
aagtttgaga ggataagaca ttggaatcgt ctaaccagga ggcggaggaa ttccctagac 420
agttaaaagt ggccggaatc ccggtaaaaa agattaaaat ttttttgtag agggagtgct 480
tgaatcatgt tttttatgat ggaaatagat tcagcaccat caaaaacatt caggacacct 540
aaaattttga agtttaacaa aaataacttg gatctacaaa aatccgtatc ggatttttctc 600
taaatataac tagaattttc ataactttca aagcaactcc tcccctaacc gtaaaacttt 660
tcctacttca ccgttaatta cattccttaa gagtagataa agaaataaag taaataaaag 720
tattcacaaa ccaacaattt atttctttta tttacttaaa aaaacaaaaa gtttatttat 780
tttacttaaa tggcataatg acatatcgga gatccctcga acgagaatct tttatctccc 840

```
tggttttgta ttaaaaagta atttattgtg gggtccacgc ggagttggaa tcctacagac    900
gcgctttaca tacgtctcga gaagcgtgac ggatgtgcga ccggatgacc ctgtataacc    960
caccgacaca gccagcgcac agtatacacg tgtcatttct ctattggaaa atgtcgttgt   1020
tatccccgct ggtacgcaac caccgatggt gacaggtcgt ctgttgtcgt gtcgcgtagc   1080
gggagaaggg tctcatccaa cgctattaaa tactcgcctt caccgcgtta cttctcatct   1140
tttctcttgc gttgtataat cagtgcgata ttctcagaga gcttttcatt caaaggtatg   1200
gagttttgaa gggctttact cttaacattt gtttttcttt gtaaattgtt aatggtggtt   1260
tctgtggggg aagaatcttt tgccaggtcc ttttgggttt cgcatgttta tttgggttat   1320
ttttctcgac tatggctgac attactaggg ctttcgtgct ttcatctgtg ttttcttccc   1380
ttaataggtc tgtctctctg gaatatttaa ttttcgtatg taagttatga gtagtcgctg   1440
tttgtaatag gctcttgtct gtaaaggttt cagcaggtgt ttgcgtttta ttgcgtcatg   1500
tgtttcagaa ggcctttgca gattattgcg ttgtacttta atattttgtc tccaaccttg   1560
ttatagtttc cctcctttga tctcacagga acccttttctt ctttgagcat tttcttgtgg   1620
cgttctgtag taatatttta attttgggcc cgggttctga gggtaggtga ttattccagt   1680
gatgtgcttt ccctataagg tcctctatgt gtaagctgtt agggtttgtg cgttactatt   1740
gacatgtcac atgtcacata ttttcttcct cttatccttc gaactgatgg ttctttttct   1800
aattcgtgga ttgctggtgc catattttat ttctattgca actgtatttt agggtgtctc   1860
tttctttttg atttcttgtt aatatttgtg ttcaggttgt aactatgggt tgctagggtg   1920
tctgccctct tcttttgtgc ttctttcgca gaatctgtcc gttggtctgt atttgggtga   1980
tgaattattt attccttgaa gtatctgtct aattagcttg tgatgatgtg caggtatatt   2040
cgttagtcat atttcaattt caag atg cag atc ttt gtc aag act ctc acc       2091
                         Met Gln Ile Phe Val Lys Thr Leu Thr
                          1               5

ggt aag acc atc act ctc gag gtc gag agc tct gac acc att gac aat      2139
Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn
 10                  15                  20                  25

gtt aaa gct aag atc cag gac aag gaa ggg att ccc ccc gac cag cag      2187
Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln
             30                  35                  40

cgt ctg atc ttc gca gga aag cag ctt gag gac ggc cga acc ctt gcc      2235
Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala
          45                  50                  55

gat tac aac atc cag aaa gaa tct acc ctc cac ctt gtt ctc cgt ttg      2283
Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu
      60                  65                  70

agg ggt ggc atg caa atc ttt gta aaa aca cta act gga aag aca att      2331
Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile
  75                  80                  85

aca ttg gaa gtt gag agc tcg gac acc att gac aac gtc aag gcc aag      2379
Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys
 90                  95                 100                 105

atc cag gac aag gaa gga att ccc cct gac cag cag agg ctt atc ttc      2427
Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe
                110                 115                 120

gct ggt aag cag ctg gag gat ggc agg acc ttg gct gat tac aat att      2475
Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile
            125                 130                 135

caa aag gaa tcg acc ctg cat ttg gtg ctt cgt cta aga gga ggc atg      2523
```

```
Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met
        140                 145                 150

caa atc ttt gtg aaa acc ctt aca ggt aaa acc att act ctg gaa gtg     2571
Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val
    155                 160                 165

gaa agc tcg gac acc att gac aat gtg aag gct aag atc cag gac aag     2619
Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys
170                 175                 180                 185

gag gga att cca cct gac cag cag agg ttg atc ttt gcc ggt aag cag     2667
Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln
                190                 195                 200

ctg gaa gat ggt cgt act ctc gcc gat tac aat att cag aag gaa tcg     2715
Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser
            205                 210                 215

acc ctt cac ctg gtg ctc cgt ctc cgc ggt ggc ttt taggtttggg          2761
Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Phe
        220                 225

tgttatttgt ggataataaa ttcgggtgat gttcagtgtt tgtcgtattt ctcacgaata   2821
aattgtgttt atgtatgtgt tagtgttgtt tgtctgtttc agaccctctt atgttatatt   2881
tttcttttcg tcggtcagtt gaagccaata ctggtgtcct ggccggcact gcaataccat   2941
ttcgtttaat ataaagactc tgttatccgt tatgtaattc catgttatgt ggtgaaatgt   3001
ggatgaaatt cttagaaatt attattgtaa tttgaaactt ccttcgtcaa taatctgcac   3061
aacacattta ccaaaaaaaa aa                                           3083

<210> 2
<211> 2064
<212> DNA
<213> Pinus radiata

<220>
<221> 5'UTR
<222> (1)...(2064)

<221> intron
<222> (1196)...(2033)

<400> 2
aaaacccctc acaaatacat aaaaaaaatt ctttatttaa ttatcaaact ctccactacc     60
tttcccacca accgttacaa tcctgaatgt tggaaaaaac taactacatt gatataaaaa    120
aactacatta cttcctaaat catatcaaaa ttgtataaat atatccactc aaaggagtct    180
agaagatcca cttggacaaa ttgcccatag ttggaaagat gttcaccaag tcaacaagat    240
ttatcaatgg aaaaatccat ctaccaaact tactttcaag aaaatccaag gattatagag    300
taaaaaatct atgtattatt aagtcaaaaa gaaaaccaaa gtgaacaaat attgatgtac    360
aagtttgaga ggataagaca ttggaatcgt ctaaccagga ggcggaggaa ttccctagac    420
agttaaaagt ggccggaatc ccggtaaaaa agattaaaat ttttttgtag agggagtgct    480
tgaatcatgt tttttatgat ggaaatagat tcagcaccat caaaaacatt caggacacct    540
aaaattttga agtttaacaa aaataacttg gatctacaaa aatccgtatc ggatttctc     600
taaatataac tagaattttc ataactttca aagcaactcc tcccctaacc gtaaaacttt    660
tcctacttca ccgttaatta cattccttaa gagtagataa agaaataaag taaataaaag    720
tattcacaaa ccaacaattt atttctttta tttacttaaa aaaacaaaaa gtttatttat    780
tttacttaaa tggcataatg acatatcgga gatccctcga acgagaatct tttatctccc    840
```

tggttttgta ttaaaaagta atttattgtg gggtccacgc ggagttggaa tcctacagac 900
gcgctttaca tacgtctcga gaagcgtgac ggatgtgcga ccggatgacc ctgtataacc 960
caccgacaca gccagcgcac agtatacacg tgtcatttct ctattggaaa atgtcgttgt 1020
tatccccgct ggtacgcaac caccgatggt gacaggtcgt ctgttgtcgt gtcgcgtagc 1080
gggagaaggg tctcatccaa cgctattaaa tactcgcctt caccgcgtta cttctcatct 1140
tttctcttgc gttgtataat cagtgcgata ttctcagaga gcttttcatt caaaggtatg 1200
gagttttgaa gggctttact cttaacattt gtttttcttt gtaaattgtt aatggtggtt 1260
tctgtggggg aagaatcttt tgccaggtcc ttttgggttt cgcatgttta tttgggttat 1320
ttttctcgac tatggctgac attactaggg ctttcgtgct ttcatctgtg ttttcttccc 1380
ttaataggtc tgtctctctg gaatatttaa ttttcgtatg taagttatga gtagtcgctg 1440
tttgtaatag gctcttgtct gtaaaggttt cagcaggtgt ttgcgtttta ttgcgtcatg 1500
tgtttcagaa ggcctttgca gattattgcg ttgtacttta atattttgtc tccaaccttg 1560
ttatagtttc cctcctttga tctcacagga acccttttctt ctttgagcat tttcttgtgg 1620
cgttctgtag taatatttta attttgggcc cgggttctga gggtaggtga ttattccagt 1680
gatgtgcttt ccctataagg tcctctatgt gtaagctgtt agggtttgtg cgttactatt 1740
gacatgtcac atgtcacata ttttcttcct cttatccttc gaactgatgg ttctttttct 1800
aattcgtgga ttgctggtgc catattttat ttctattgca actgtatttt agggtgtctc 1860
tttctttttg atttcttgtt aatatttgtg ttcaggttgt aactatgggt tgctagggtg 1920
tctgccctct tcttttgtgc ttctttcgca gaatctgtcc gttggtctgt atttgggtga 1980
tgaattattt attccttgaa gtatctgtct aattagcttg tgatgatgtg caggtatatt 2040
cgttagtcat atttcaattt caag 2064

<210> 3
<211> 1226
<212> DNA
<213> Pinus radiata

<220>
<221> 5'UTR
<222> (1)...(1266)

<400> 3
aaaacccctc acaaatacat aaaaaaaatt ctttatttaa ttatcaaact ctccactacc 60
tttcccacca accgttacaa tcctgaatgt tggaaaaaac taactacatt gatataaaaa 120
aactacatta cttcctaaat catatcaaaa ttgtataaat atatccactc aaaggagtct 180
agaagatcca cttggacaaa ttgcccatag ttggaaagat gttcaccaag tcaacaagat 240
ttatcaatgg aaaaatccat ctaccaaact tactttcaag aaaatccaag gattatagag 300
taaaaaatct atgtattatt aagtcaaaaa gaaaaccaaa gtgaacaaat attgatgtac 360
aagtttgaga ggataagaca ttggaatcgt ctaaccagga ggcggaggaa ttccctagac 420
agttaaaagt ggccggaatc ccggtaaaaa agattaaaat ttttttgtag agggagtgct 480
tgaatcatgt tttttatgat ggaaatagat tcagcaccat caaaaacatt caggacacct 540
aaaattttga agtttaacaa aaataacttg gatctacaaa aatccgtatc ggattttctc 600
taaatataac tagaattttc ataactttca aagcaactcc tcccctaacc gtaaaacttt 660
tcctacttca ccgttaatta cattccttaa gagtagataa agaaataaag taaataaaag 720
tattcacaaa ccaacaattt atttctttta tttacttaaa aaaacaaaaa gtttatttat 780
tttacttaaa tggcataatg acatatcgga gatccctcga acgagaatct tttatctccc 840
tggttttgta ttaaaaagta atttattgtg gggtccacgc ggagttggaa tcctacagac 900
gcgctttaca tacgtctcga gaagcgtgac ggatgtgcga ccggatgacc ctgtataacc 960
caccgacaca gccagcgcac agtatacacg tgtcatttct ctattggaaa atgtcgttgt 1020
tatccccgct ggtacgcaac caccgatggt gacaggtcgt ctgttgtcgt gtcgcgtagc 1080
gggagaaggg tctcatccaa cgctattaaa tactcgcctt caccgcgtta cttctcatct 1140
tttctcttgc gttgtataat cagtgcgata ttctcagaga gcttttcatt caaaggtata 1200
ttcgttagtc atatttcaat ttcaag 1226

<210> 4
<211> 485
<212> DNA

<213> Pinus radiata

<220>
<221> 5'UTR
<222> (1)...(431)

<221> TATA_signal
<222> (350)...(356)

<221> CAAT_signal
<222> (326)...(333)

<400> 4
agtaaaattg gcccatgtag gactaagtca aaatcaaaat tccatctcta aaagcggaac 60
tttgtcccct gaaaattttg actaatttcc aaccaaaaaa aagtgggggа aaatataaaa 120
ctctaactaa taaaacaata atcaccaaaa atctatcacc aaaaatgaaa aaagattttg 180
aatactaggc catatgagct acacaaattt caaaagtatc ttacacttat tacgcacccg 240
gatgtcccca ctttcgaaaa acccgtttca agcctttcac gaaagtccaa cggtcagaaa 300
attcaaaatg actgtttgag gcagagccaa tctaggacca cgctccattt atatatggcc 360
tctgcttctc tcgaccctta gagtcctctg ctctgcgaat cttgttgtta gttactgtgt 420
acgctgtaac aatggatgcc tatgagaagt tggagaaggt gggagaagga acctatggga 480
aggtg 485

<210> 5
<211> 246
<212> DNA
<213> Pinus radiata

<220>
<221> 5'UTR
<222> (1)...(167)

<221> TATA_signal
<222> (185)...(191)

<400> 5
tgagaacatg ataagctgtg taaattcatg ctagtcacca taacttttct cattgctttt 60
catccacact gttgattcat tcattatata agatcagatt cgtatgatat acaggcaacc 120
atagaaacaa ccagcaaagt tactagcagg aaatccaact aggtatcatg aagactacca 180
acgcaggctc gataatgttg gtgctcatta tttttgggtg ctgtttcatt ggggtcatag 240
ctacat 246

<210> 6
<211> 600
<212> DNA
<213> Pinus radiata

<220>
<221> 5'UTR
<222> (1)...(167)

<221> TATA_signal
<222> (471)...(477)

<221> CAAT_signal
<222> (444)...(451)

<400> 6
caccaattta atgggatttc agatttgtat cccatgctat tggctaagcc atttttctta 60
ttgtaatcta accaattcca atttccaccc tggtgtgaac tgactgacaa atgcggcccg 120
aaaacagcga atgaaatgtc tgggtgatcg gtcaaacaag cggtgggcga gagaacgcgg 180
gtgttggcct agccgggatg ggggtaggta gacggcgtat taccggcgag ttgtccgaat 240
ggagttttcg gggtaggtag taacgtagac gtcaatggaa aaagtcataa tctccgtcaa 300
aaatccaacc gctccttcac accgcagagt tggtggccac gggaccctcc acccactcac 360
tcaatcgatc gcctgccgtg gttgcccatt attcaaccat acgccacttg actcttcacc 420
aacaattcca ggccggcttt cgagacaatg tactgcacag gaaaatccaa tataaaaggc 480
cggcctccgc ttccttctca gtagcccccа gctcattcaa ttcttcccac tgcaggctac 540
atttgtcaga cacgttttcc gccatttttc gcctgtttct gcggagaatt tgatcaggtt 600

<210> 7
<211> 591
<212> DNA
<213> Eucalyptus grandis

<220>
<221> 5'UTR
<222> (1)...(591)

<221> TATA_signal
<222> (432)...(437)

<400> 7
agtttggaat gtgttgtgtg tgatgtgatg gagagtatca gcattccaaa catgacatgg 60
ttttaactta tctgcaatgg tttctttttt attcagcgaa ctcgatggct gatgctgaga 120
gaaatgaatt gggaagtcga tcgacaatgg cagctcaact caatgatcct caggtataag 180
catttttttg gcagctctgg tcattgtgtc ttcaactttt agatgagagc aaatcaaatt 240
gactctaata ccggttatgt gatgagtgaa tcatttgctt ttagtagctt taatttatgc 300
ccccatctta gttgggtata aaggttcaga gtgcgaagat tacatctatt ttggttcttg 360
caggacacag ggattcatgc tagacacatc agcagtgttt ctacgttgga tagtggtatg 420
tacttagcta ctataaagga aattttgata gatatgtttg atatggtgct tgtacagatc 480
tatttaatgt caatgtattt gaaactatct tgtctcataa ctttcttgaa gaatacaatg 540
atgagactgg gaaccctatc tggaagaata gagtggagag ctggaaggac a 591

<210> 8
<211> 480
<212> DNA
<213> Eucalyptus grandis

<220>
<221> 5'UTR
<222> (1)...(480)

<400> 8
atgctgagag aaatgaattg ggaagtcgat cgacaatggc agctcaactc aatgatcctc 60
aggtataagc attttttgg cagctctggt cattgtgtct tcaactttta gatgagagca 120
aatcaaattg actctaatac cagttatgtg atgagtgaat catttgcttt tagtagcttt 180
aatttatgcc cccatcttag ttgggtataa aggttcagag tgcgaagatt acatctattt 240
tggttcttgc aggacacagg gattcatgct agacacatca gcagtgtttc tacgttggat 300
agtggtatgt acttagctac tataaaggaa attttgatag atatgtttga tatggtgctt 360
gtacagatct atttaatgcc aatgtatttg aaactatctt gtctcataac tttcttgaag 420
aatacaatga tgagactggg aaccctatct ggaagaatag agtggagagc tggaaggaca 480

<210> 9
<211> 308

<212> DNA
<213> Eucalyptus grandis

<220>
<221> 5'UTR
<222> (1)...(259)

<400> 9
gcccatctca ggtgcaacgg tttaactgat gtttactaca cgcaaggggg aggtatccgg 60
aaagcttgca aatcgggtaa aaacgaaaat gggcgacgtg gactcagcct gcccatgttt 120
tcggtctctc tcctggactt ccatgcccga taagggccgc caactctctc tctctctctc 180
ttttttctct acatctctct gcctgttcat gtcgcctgca agtgaagatt cgtcggagca 240
agaaggacga accgggcaca tggcggggtc ggcggtcgcg acggttctaa agggtctctt 300
cctggtgt 308

<210> 10
<211> 300
<212> DNA
<213> Eucalyptus grandis

<220>
<221> 5'UTR
<222> (1)...(251)

<400> 10
gcccatctca ggtgcaacgg tttaactgat gtttactaca cgcaaggggg aggtatccgg 60
aaagcttgca aatcgggtaa aaacgaaaat gggcgacgtg gactcagcct gcccatgttt 120
tcggtccctc tcctggactt ccatgcccga taaaggccgc caactctctc tctttttctc 180
tcacatctct ctgcctgttc atgtcgcctg caagtgaaga ttcgtcggag caagaaggac 240
gaactgggca tatggcgggg tcggcggtcg cgacggttct aaagggtctc ttcctggtgt 300

<210> 11
<211> 297
<212> DNA
<213> Eucalyptus grandis

<400> 11
gtgcaacggt ttaactgatg tttactacac gcaaggggga ggtatccgga aagcttgcaa 60
atcgggtaaa aacgaaaatg ggcgacgtgg actcagcctg cccatgtttt cggtctctct 120
cctggacttc catgcccgat aagggccgcc aactctctct ctctctctct ttttctctca 180
catctctctg cctgttcatg tcgcctgcaa gtgaagattc gtcggagcaa gaaggacgaa 240
ctgggcatat ggcggggtcg gcggtcgcga cggttctaaa gggtctcttc ctggtgt 297

<210> 12
<211> 661
<212> DNA
<213> Eucalyptus grandis

<400> 12
ctgagccatt taattcgaga gcacatcgcc caaaattatt cttcttgctg ccataactgt 60
cgaattttct cttttaggta agtaaccaat gatgcatcat gttgacaaaa aggctgatta 120
gtatgatctt ggagttgttg gtgcaaattt gcaagctgac gatggcccct cagggaaatt 180
aaggcgccaa cccagattgc aaagagcaca aagagcacga tccaaccttt ccttaacaag 240
atcatcacca gatcggccag taagggtaat attaatttaa caaatagctc ttgtaccggg 300
aactccgtat ttctctcact tccataaacc cctgattaat ttggtgggaa agcgacagcc 360
aacccacaaa aggtcagatg tcatcccacg agagagagag agagagagag agagagagag 420
agagttttct ctctatattc tggttcaccg gttggagtca atggcatgcg tgacgaatgt 480

acatattggt gtagggtcca atattttgcg ggagggttgg tgaaccgcaa agttcctata 540
tatcgaacct ccaccaccat acctcacttc aatccccacc atttatccgt tttatttcct 600
ctgctttcct ttgctcgagt ctcgcggaag agagagaaga gaggagagga gagaatgggt 660
t 661

<210> 13
<211> 336
<212> DNA
<213> Pinus radiata

<400> 13
actagtgatt tgttgagaat gagtaggcat tgctacaccc atcatcacaa gcatcatcat 60
gaggagaaga agatccattt ctcactctat tactcgaact tccttcagat taggctgtgt 120
atttctcact ctaccactcc aacttccttc aaatgctgtg agtttttgtt gtaattgccc 180
cgtctattta taatcgcagc agcactcgtc atataaagac ccgtgtgtgt gaacaacaac 240
caagtgattt gaattggaaa tgaagagcga gaatggcggt gtcatgaccg ggagcaacca 300
gcccgggccg tcgaccacgc gtgccctata gtaatc 336

<210> 14
<211> 763
<212> DNA
<213> Pinus radiata

<400> 14
actagtgatt tgttgagaat gagtaggcat tgctacaccc atcatcacaa gcatcaacat 60
gaagagaaga agacgatcca tttctcactc tatcactcca acttccttca gattaggctg 120
tgtatttctc actctaccac tccaactacc actccaactt attgccgcaa aagagagagg 180
ttcccaaact ctgtcggaat tctcccactc aaagcattaa aggaaagatc taattgctgc 240
aaaaaagaga gattcccaat atatttctca actcccttca aatgatttct cactctacca 300
ctccaactcc cttcaaatga tttctcactc taccactcca acttccttca aatgctgtga 360
gtttttgttg taattgcccc gtctatttat aatcgcagca gcactcgtca tataaagacc 420
cgtgcgtgtg aacaacaatg gcggtgtctt gactgggagc aaccgcataa agaaagtggg 480
cttcatacat taaaaaaatc tgtaaatttt acggatttgg aaaaaggaag agcaggaggg 540
acctcccgac ttgacccgag aatggcggtg tcttgaccgc gtaaagaaag tggtcttctg 600
tacccgactt gacccgaaaa aagaggaaac gttgaacgag acaatctctg ggaacttcat 660
cgaaatgaac ctcacgactt gactctttcg attgtactgt tttcattgtt cccgcgtaaa 720
acgaccagcc cgggccgtcg accacgcgtg ccctatagta atc 763

<210> 15
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 15
acggataaca gagtctttat attaaacgaa atggtattgc 40

<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 16
tgacgcggcc gcgaccgacg aaaagaaaaa tataacataa gagagtctga a 51

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 17
tatagcggcc gcgggggggg ggggggg 27

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 18
cggagaacaa ggtggagggt agattctttc 30

<210> 19
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 19
tctgcatctt gaaattgaaa tatgactaac g 31

<210> 20
<211> 363
<212> DNA
<213> Eucalyptus grandis

<400> 20
aatcgggtga aaatagggcc gccctaaatt agaattgaca acatttcttg ggcaaagtta 60
atgtaagtta catgaaaaaa aaaaaaaagg atagtttgtt ggaagtaatg gagcatttgt 120
attgtgaaat tcacgataga gctaacaaaa ataaaggtag ttggtgggtt aacccagtta 180
aaaaagaaca ataatttgaa gagaggagag agagagagag gaggggggaga gcatttcgat 240
aaattcacta gaaaaaatgc gtgttttagt ataaatgaga gtggaaatag ggccatctag 300
ggaacgatcg atcgcccctg cacccggcca tctggagagt ctgtttatac ttctctccgg 360
ctt 363

<210> 21
<211> 839
<212> DNA
<213> Pinus radiata

<220>
<221> misc_feature

<222> (1)...(839)
<223> n = A,T,C or G

<400> 21
gtatggagtt ttgaagggct ttactcttaa catttgtttt tctttgtaaa ttgttaatgg 60
tggtttctgt gggggaagaa tcttttgcca ggtccttttg ggtttcgcat gtttatttgg 120
gttatttttc tcgactatgg ctgacattac tagggctttc gtgctttcat ctgtgttttc 180
ttcccttaat aggtctgtct ctctggaata tttaattttc gtatgtaagt tatgagtagt 240
cgctgtttgt aataggctct tgtctgtaaa ggtttcagca ggtgtttgcg ttttattgcg 300
tcatgtgttt cagaaggcct ttgcagatta ttgcgttgta ctttaatatt ttgtctccaa 360
ccttgttata gtttccctcc tttgatctca caggaaccct ttcttctttg agcatttttct 420
tgtggcgttc tgtagtaata ttttaatttt gggcccgggt tctgagggta ggtgattatt 480
cncagtgatg tgctttccct ataaggtcct ctatgtgtaa gctgttaggg tttgtgcgtt 540
actattgaca tgtcacatgt cacatatttt cttcctctta tccttcgaac tgatggttct 600
ttttctaatt cgtggattgc tggtgccata ttttatttct attgcaactg tattttaggg 660
tgtctctttc tttttgattt cttgttaata tttgtgttca ggttgtaact atgggttgct 720
agggtgtctg ccctcttctt ttgtgcttct ttcgcagaat ctgtccgttg gtctgtattt 780
gggtgatgaa ttatttattc cttgaagtat ctgtctaatt agcttgtgat gatgtgcag 839

<210> 22
<211> 881
<212> DNA
<213> Eucalyptus grandis

<400> 22
acgtgacgat gctcgagtct cgcgttctcc tctctcttgt tctgcaaaac agaaaagaga 60
gaatggaggt tggcctctct caattacgtg gacgccaatg agataactca ggtgggcgac 120
aaaacaaacg cctcttgatt tcctcaaacc ccaaaccgaa tccctcgtca aggggcaagg 180
cttttggtcc cgcggcccca cggatcgctc gttcccgtct cgccacgtcg cgtcgcagcg 240
tgtcgagcaa acagaggggt ccgagcgact ataaaatccc gacgccatcg acaccacagt 300
ccatcgaaaa ccttgttcaa ttcccaagtg aaagtgagta actgtgaacg aagagttgaa 360
ctttgcatct cggcgtgtgg attcaagagg aagcagcaaa gtggaaatgg acaactccaa 420
gatgggcttc aatgcagggc aggccaaggg ccagactcag gagaagagca accagatgat 480
ggataaggca tccaacactg ctcaatctgc aagggattcc atgcaagaga ctggtcagca 540
gatgaaggcc aaagcccagg gtgctgctga tgcagtgaag aatgccaccg ggatgaacaa 600
atgaagagct caagacatga atgaataaat aattaagctc tggttatcat ttgcttttcc 660
ggtcgtttgt tgtcctgttt ttccttgtca agagcttatt atgagggtcc ttttgctctt 720
tccttagttc tttttgtttc ttggttgttc catgaagaga gcaactctct gtgtttgaga 780
gtactcatct cgcttcataa ggtctcagta tgtagttgcc tttcgagaat gttatgttct 840
ctctcataat gctattctga ttttataaaa aaaaaaaaaa a 881

<210> 23
<211> 350
<212> DNA
<213> Eucalyptus grandis

<400> 23
ctatagggca cgcgtggtcg acggcccggg ctggtccttt cttacaaaaa gcaaaattct 60
tataattttt tttgatataa taaaaatgat ccataaactt ttgcttaatg tgcaacgtaa 120
accataatat attcaacgtg atgcttaaac tttaatcgag tatgcaatgt agtccataat 180
atattcaata tgatccttca atccaattga agtgtgcaat gtggtcgcta gatttttta 240
tgtattcaac ttagtcttta agctaccaac cttccaataa tttatgtttt agaaataata 300
tcgaacatct tttatattat tcaaggaata aaacgaacat gcatcaaaag 350

<210> 24
<211> 49
<212> DNA

<213> Eucalyptus grandis

<400> 24
actatagggc acgcgtggtc gacggcccgg gctggtactt tttttttct 49

<210> 25
<211> 909
<212> DNA
<213> Eucalyptus grandis

<400> 25
cagggtaaag aaaatggaat atttgcttgg ccccccagct ttgaaagttg ctgtaagaac 60
acactcacct tgcatttata cgatggttgt gagcagtgca ggctggtggt gctgcaaatt 120
tatgatgctg atgtgatagg cagatgaatg gcagttgagc taagttaaag ccctcataca 180
tagatcagag caggaggagt agtatatata ggcatcttgg caagtcccta aaagagcggc 240
ttcgtgtatt cccacatatt cctctctcgt tagaacgttc agaaatgggt ggccctttga 300
ctcttgatgc agaggttgag gttaagtctc ctgcagacaa gttctgggtg agcgtgagag 360
actccaccaa actgttccca aagatcttcc cggaccagta caagaatatt gaagtccttg 420
agggagatgg gaaggctcct ggctcagttc gcctcttcac gtatggtgaa ggttctccac 480
ttgttaaagt atcaaaggag aagattgatg gtgtggacga agcagacaag gtcgtgacct 540
acagcgttat agacggtgat ctcctgaagt actacaagaa tttcaatggc agcatcaagg 600
taattcctaa aggagacgga agcttggtga aatggtcgtg tgggtttgag aaggcaagcg 660
atgaaattcc tgatccccac gtaatcaagg acttcgcaat ccagaatttc aaagagcttg 720
atgagttcat cctcaaggca tagatgccgc caatcgtcta tccggatttg cactaaatat 780
caataaaata atgcggagct ggactccgca cttctatatg catctagtat gagagtcccc 840
tgctgtctct gtttgtattc acttgaaggg ttttctatta agctctcttt actgcctccg 900
aaaaaaaaa 909

<210> 26
<211> 430
<212> DNA
<213> Eucalyptus grandis

<400> 26
tggagcttga gatagatcga ccgagagatc ccagcggaaa tagaagattt cctgatacca 60
tcgatccttc ttctccaatg gctgcgaatt tcgtcattcc gaccaaaatg aaggcttggg 120
tgtaccgtga gcacggaaac gtcgccgacg tattgggatt ggacccggaa ctcaaggtcc 180
ctgaattgca agaaggccaa gtgctggtta aagttcttgc cgcagcgctc aatccagtcg 240
acgccgcgag aatgaagggg gttatcaagc tcccgggctt ttctctaccg gccgtgccag 300
gttacgatct cgccggcgtt gtggtaaagg tgggccgcga agtgaaggag ctcaagatcg 360
gggacgaggt atatggattt atgtttcacg ccaagaaaga cgggacgctg gctgagtacg 420
cagccgtgga 430

<210> 27
<211> 1253
<212> DNA
<213> Eucalyptus grandis

<400> 27
gcttgagata gatcgactga gagatcctag tggaaataga agatttcctg ataccatcga 60
tccattcttc tccaatggct gcgaatttcg tcattccaac caaaatgaag gcttgggtgt 120
accgtgagca cggagacgtc gccaacgtat tgggattgga cccggaactc aaggtccctg 180
aattgcaaga aggccaagtg ctggttaaag ttcttgccgc ggcgctcaat ccaatcgaca 240
ccgcgagagt gaaggggctt atcaagctcc cgggcttttc tctaccggcc gtgccaggtt 300
acgatctcgc cggcgttgtg gtgaaggtgg gccgcgaagt gaaggagctc aaggtcgggg 360
acgaggtata tggatttatg tttcacgcca agaaagacgg gacgctggct gagtacgcag 420
ccgtggaaga gtcgttcttg gctttgaagc ccaagaagct gcgtttcggg gaggctgctt 480

ctctgccggt ggtcattcag accgcctatg gaggccttga aagagctggc ctctctcatg 540
gcaagtccct cctcgtctta ggtggtgctg gtggcgtcgg cacactcata atacagctag 600
ctaaggaagt ttttggtgca tcaagagtag cagctacatc cagcactggg aagctagagt 660
tgttgaagag cttgggtgct gatctggcca ttgactacac caaagtcaac tttgaagacc 720
tcccagaaaa gtttgatgtt gtctacgata cagttgggga aattgagcgg gcagcgaagg 780
ctgtgaagcc aggagggagc atcgtgacga tcgtaaaaca aaacaagaca ttacccccgc 840
ctgctttctt ttttgcagta acttcgaacc gttcgacctt ggagaagttg aagcccttct 900
tggagagcgg gaaggtgaag ccggtgatcg accccaagag cccgttccca ttttcgcaag 960
ccattgaggc cttctcgtat cttcaaaccc gccgggcaac tggaaaactc gtgattcacc 1020
ccgtcccatg atacacaaac gagaaagaaa taaagcgtcc acatggatct gccttaatca 1080
cgagtcctta attagtagtc gatggtgctt gctgtttgtc tccgtacatt cagcttctct 1140
ttgcatagta gtttctacat agtgcgtgta gagaagcaag tggatgtaca agtaaaataa 1200
ttacttttc tataaacaat attacaaact caaaaaaaaa aaaaaaaaaa aaa 1253

<210> 28
<211> 99
<212> DNA
<213> Eucalyptus grandis

<400> 28
gatagatcga ccgagagatc ccagcggaaa tagaagattt cctgatacca tcgatccatt 60
cttctccaat ggctgcgaat ttcgtcattc cgaccaaaa 99

<210> 29
<211> 927
<212> DNA
<213> Eucalyptus grandis

<400> 29
cgacgtcgca tgctcccggc cgccatgcgg ccgcgggaat tcgattacta tagggcacgc 60
gtggtcgacg gcccgggctg gtactctcac taattcttta gttttccaat ttagcccctt 120
ctgtaattgc tcatcttctt taccaaattc tctaatttgg ccggcgaagg gctgacaagg 180
gattggtcat gtcaccctca ccaaaggttg ccgaaggtcc ggtgacctca gctgacggcc 240
acctacacca aatctagctc actagcagcc taagcccttc atcaactcta gtgaaaggtt 300
ttgagtattt tttaataaaa aatatttaaa aaatatatag cgagagctca ttacaaaaaa 360
attttaaaaa aaaatctaaa cattacttga actcaaagtg actttataaa gagtttttac 420
caaaggatct tggtttcatc atttgcacta cacccaaaac ccaatttcta agttaaatca 480
aacccactgt ctaatagaga taaggtaaat gttataaacc aaattccaaa attccgaagc 540
actaaatata tttgctgatc ttataatcgc caattgagag ggtctcattc tccaagggat 600
tgtgacatat tagtaattga tagggtctca tccgtaggac tccgactcag ccgcgccacg 660
tgactggatc gctgaacggc gcggaaccag aggagcgtga ttacctaata ttttctccta 720
ccttggcctt gagattgaat ttcagaaaaa gaaaaagaaa aaggaacaac ttcgccgact 780
gttctataaa atgcatgcgc caccccgacc cccacccacg catcacatcc atccagcctc 840
cacgacagac gcataaacac aacacacgtc ggttagagag agagagagag agagagagag 900
agagagagag atgcttggac agttgtc 927

<210> 30
<211> 411
<212> DNA
<213> Eucalyptus grandis

<400> 30
actatagggc acgcgtggtc gacggcccgg gctggtctga aactgtcgct cggcgatgca 60
taccaaaggc tgaaggtatc agaatctaat gcagcttatg taaaagcgcg atcaatttat 120
tgaccccgac gaccttgact ccatacttca cgcctcagct ttgtgttgga tggtcttgac 180
ctctctcacc ctaaaaggta gctcaaaaga atgagacttt ccgtcatact tataaaccga 240
ccaccagcct ctttcacaac cgacatggga caacctcaaa tagaattttt aacaacaccc 300

ttgcacgctc tttctatcca ctttattatg ccatcacatg agcgttttcc acgcgtaaat 360
cggctaccac ccactttcac acggcggcga aacgagaaaa aggtcctacc t 411

<210> 31
<211> 178
<212> DNA
<213> Eucalyptus grandis

<400> 31
cgagtcagca gaaacccagt tacactccgc ccaaacggaa gctaaacctg atgggccata 60
cgatttcttt cactgagcct cttgcttttc ctccggaatc tcacggcacc ggaatgccgg 120
aggaacttgg gaagaaccaa tgatgcctgg tcactgagtg atcgatgaat gcaatagt 178

<210> 32
<211> 178
<212> DNA
<213> Eucalyptus grandis

<400> 32
gtccaatgtc ctgtcaaagg aggaaagatg actatggccc cggcgccggc ggggactgca 60
tgggatttag tatgttgatt gagtacccgt cgccaccacc ttcaagtaaa tcaggagtca 120
gcagaaaccc agtacactcg ccaaacggag ctaaacctga tggccatacg atttcttt 178

<210> 33
<211> 178
<212> DNA
<213> Eucalyptus grandis

<400> 33
gcatgggatt tagtatgttg attgagtacc cgtcgccacc accttcaagt aaatcaggag 60
tcagcagaaa cccagtacac tcgccaaacg gagctaaacc tgatggccat acgatttctt 120
tcactgagcc tcttgctttt cctccggaat ctcacggcac cggaatgccg gaggcaac 178

<210> 34
<211> 1274
<212> DNA
<213> Eucalyptus grandis

<400> 34
ctatagggca cgcgtggtcg acggcccggg ctggtccttt cttacaaaaa gcaaaattct 60
tataatttt tttgatataa taaaaatgat ccataaactt ttgcttaatg tgcaacgtaa 120
accataatat attcaacgtg atgcttaaac tttaatcgag tatgcaatgt agtccataat 180
atattcaata tgatccttca attttaattg aatgtgcaat gtggtcgcta gatttttta 240
tgtattcaac ttagtcttta agctaccaac cttccaataa tttatgttta gaaataatat 300
cgaacatctt ttatattatt caaggaataa aacgaacatg catcaaaagt ttaaatatat 360
caaataaaat aaaattttaa gaattatatt acatattaaa attaaagttc atgattaaat 420
tgaaataaaa taaaaattta aaaatcacgt tgtatgttgt gccgaaacaa aattcagtga 480
cttgtggtgt caattttctt aggtggagct ccacaagcat tgagatggag tgttccttcc 540
gccgaggttt tcattgcgtg gctcaaaacg gtggcgcgtt ttgcacgaca cgagatgcct 600
cgattgccgc atcgtgtagg cgacgcaacg gaaaaacgcg ttgccgtggc gtctatccgg 660
ggtttcgtct ccgatgcggc acgtagccta taaatgcgca cgatctcccg gtctgccaat 720
tcgctatcga ttgcagaaga aaactcaaac cctaggcgct ctctctccgt tcgacctctc 780
gaagttctcc tctcttcgcg tcaagatgca aatctttgtg aaaaccctta ctggcaagac 840
aatcaccctc gaggtggaaa gctcggacac agtcgataat gtgaaagcaa aaatccagga 900
caaggaaggg atccctccgg accagcagag gcttatcttt gctggcaagc agctggaaga 960
tggccgaacc ttggccgatt ataacattca gaaggagtcc accctccact tggtgctccg 1020
tctcagggga ggcatgcaaa tttttgtgaa gactcttact ggcaagacaa tcaccctcga 1080

ggtggaaagc tccgacacag ttgataatgt gaaagcaaaa atccaggaca aggaagggat 1140
ccctccggac cagcagaggc ttatctttgc tggcaagcag ctggaagatg gccgaacctt 1200
ggccgattat aacattcaga aggagtccac cctccacttg gtgctccgtc tcaagggagg 1260
catgcaaatc tttg 1274

<210> 35
<211> 795
<212> DNA
<213> Eucalyptus grandis

<400> 35
aaaaatacag gctttcgaaa gctagtgcgg tataaataac ctgggaaaag caagccgctt 60
gagctttagt ttcagtcagc catggccact cacgcagctc ttgctccctc aaccctcccc 120
gccaatgcca agttctctag caagagctcc tctcactcct tccccactca atgcttctct 180
aagaggctcg aggtggcgga attctcaggc cttcgtgctg gatcgtgtgt gacttatgcg 240
aagaatgccg gggagggatc cttcttcgat gctgtggctg ctcagctcac tcccaagact 300
tcagcaccag ctccagctaa gggagagact gtcgctaaac tgaaggtggc aatcaatggt 360
ttcggtcgca ttggtcggaa cttccttaga tgctggcacg ggagaaagaa ctcgcccctt 420
gatgtcattg ttgtcaatga cagcggtggt gtcaaaaatg cttcacattt gctgaagtat 480
gattccatgc tggggacttt caaagctgat gtgaaaattg tggacaatga gaccatcagc 540
gtcgatggga agcccgttaa ggtcgtctct aaccgggacc ctctcaagct cccctgggct 600
gagctcggca tcgacattgt cattgaggga actggagtct tcgtggatgg ccctggtgct 660
ggaaaacata ttcaagctgg tgccaagaaa gttatcatca ctgcaccagc aaaaggcgct 720
gatataccca cctacgtcta tggtgtgaat gagacagatt attcgcatga agttgctaac 780
ataatcagca atgct 795

<210> 36
<211> 1200
<212> DNA
<213> Eucalyptus grandis

<400> 36
aaaatatcca tcgacagcat caccccgctt agagaacggt gtctcggctt ctcacaatgt 60
ctatagccga atgtacaaaa tcggcataat gttctataat atagcggact ttacagatga 120
gcattcaaat acgtacgccg tactcgattc ccattcgatt gttcattcat ccgcatgcaa 180
atttcataga gataatatct gtgcacgtcc ttagattaag aacaaccaaa gagtatctgg 240
tggaagtttg aagcatgacc accgaagtca gatggaacaa acaaggtggg tggtggggat 300
atagtggaca aaggaacgag aggtgaatag gaaaaggaga aggcaagatg cgggagatag 360
gatttacgtg gcgagcggcg attgcacgca tggtccaccc caccctcaac ctcaaacttt 420
cgaaaatgca acgggcatca gggtggcgat gaaggagacg atggagatat tgttgctttc 480
tccccccaaa aaacatcatc caatccatcc ccattcctca tcttcaccac aaggagtctg 540
aagctctcct tcaccggtcc gtcgctttct ctcttatctt cttcttctcc ctcctcttct 600
cgttcttcct tcgaccgttc tctcggtatc gtgaatttat tgcggggtgg ttcgcatgct 660
ataaattcca cagcaacgag ggccccttgc cacaatgtcg acgtctccgg ttagcagctg 720
gtgcgccacc tccttctccc ctgcccattc ctcgctcaag agagccgccg gcctacggcc 780
ctctctctcc gcccgcctcg gcccttcctc ctcctcctcc tccgtctctc ctccgaccct 840
catccgtaac gagcccgttt tcgccgcccc cgcccctgtc atcaacccca cttggacaga 900
agagatgggc aaggactatg acgaggccat tgaggctctc aagaaactcc tcagtgagaa 960
gggggacctg aaagccacag cagccgcaaa agtggagcaa ataactgcgg agttgcaaac 1020
tgcttcccca gacatcaagc catccagctc cgttgacaga atcaaaactg gcttcacctt 1080
cttcaagaag gagaaatacg acaagaaccc tgctttatat ggtgaactgg caaagcagag 1140
tccaaagttc atggtgtttg cttgctcgga ctcgagagtg tgcccatctc atgtgctgga 1200

<210> 37
<211> 648
<212> DNA
<213> Eucalyptus grandis

<400> 37
cgacggactc ctttcacgat atcgaaacga ggaaacggag gagaagcaga agaaagaaga 60
tgaagaaagg cagatggttg gtgatggatg aaactgtcgg gaagctggga gcttcaggga 120
gttctattta tggggcgaaa caggggaggg gaaaccgaat ttaccaagat gcccttcttg 180
gtgggattgg acatggagct gcacgaccgt cgtcccatca cgaagagtct tgctcttcgg 240
tacacatgca atcgtcggcg aaccgacctt atccgaccgg ttccaagctt gtcctggtaa 300
aaggtttcga accttggaaa aggcttaaga gatgtatcgg tgccttaacc attattccat 360
gttcacataa tatttggccc ggttttcagg tcaattttgg agtagcccgg ttcggttcta 420
gtcccgctcc cgattcaaaa attcattggg aacaaatttt gacactgtct ggtatttttg 480
gtctaagacc ctacccaatt ttagaactgt acacccttgc tttatcccaa aataaaattg 540
tcaattagtc aacttttcac acttgatgat cgattaagta gatggatgac atggtctttt 600
accagcccgg gccgtcgacc acgcgtgccc tatagtgagt cgtattac 648

<210> 38
<211> 288
<212> DNA
<213> Eucalyptus grandis

<400> 38
gattgtaata cgactcacta tagggcacgc gtggtcgacg gcccgggctg gtatcgtgaa 60
agaagtccgt cgacgacaat ggccgagaag agcaaggtcc tgatcatcgg agagaagagc 120
aaggtcctga tcatcggaga gaagagcaag gtcctgatca tcggagagaa gagcagggtc 180
cttatcatcg gagaatcgaa ttcccgcggc cgccatggcg gccgggagca tgcgacgtcg 240
ggcccaattc gccctatagt gagtcgtatt acaattcact ggccgtcg 288

<210> 39
<211> 382
<212> DNA
<213> Eucalyptus grandis

<400> 39
acagcaatct catctgatga ttcttcagtt cggagctcag aggatacatc atctatagct 60
gaattgagct gtgcaatctt ctcggcaagc accttcctcg ttttctgaaa atcatcagat 120
tttaaggtga atccatattt cgcagatggc catgttactg ctacactctc ttcacagcat 180
acatgaagga ggtcacatag caagcataca taggacctca tatacaaata tgacagcaga 240
ccagcccggg ccgtcgacca cgcgtgccct atagtagtag tggggaagga gtgagaggag 300
ctcttgatga ggaatgtcgg cttttcttcc atcagttgat gttccgggtt cctagtcatt 360
atgccgatgg tggccactcc ag 382

<210> 40
<211> 986
<212> DNA
<213> Eucalyptus grandis

<400> 40
aaatacaaac tggtttaata ttcaactcag ataattacat gacaccacct aaataatgga 60
aagtcaagca aatagacata ttatccccac acataatcaa ctatattcat gactggagag 120
gtgctagatg gtatagagtc cctagttatt atttattttt ttgggcccga gaagatcctg 180
atggatctat gctgtttgat actttcagat ttgttttgtc tacagctcaa ataaattagt 240
gcttgggttt tgatatatta tctaatctga tacaagtctt tgtcctggcc aatttttgca 300
gagtttcctg caaaacagtg cactaaagct tccagaggac ctcatgccat gcccaagggc 360
accacctatg atggaacgga gaatcaaacc acagactgaa caggcgttga aatgccccag 420
atgtgattct acaaacacaa aattctgtta ctataacaac tacaatcttt cacaacctcg 480
ccatttctgc aagacctgca ggcgatactg gaccaaagga ggtgccttac gtaacgttcc 540
tgttggtggg ggttgcagaa agaataaacg agccaagcga gcagtagacc atcctgtctc 600
tgctcagaat gaagcatcca cctctgcagc cccaggcaac gaagtacctg accggtctcc 660

ctttgagcca ccatcttcaa aatccattta ctatgggga gaaaacatga acttaaccgg 720
tctccccttt agcagaattc agcaggaccg agctgcattg gcccactgca actcttcttc 780
ctttctagga atgtcatgtg gcacccaatc ggcctctctg gaaccacatc tttcggcttt 840
aaatacattt aattcattca agtctaacaa tcctggtctg gattttccta gcttaagcac 900
agaccagaat tcactgtttg agaccagcca gccacaactg tcaagagcaa tggcatctgc 960
cctttttct atgccaatgg ctcctg 986

<210> 41
<211> 313
<212> DNA
<213> Pinus radiata

<400> 41
aaaggaaaat tcaaagatct ttagccaatt tttgttgttg tgaccttgaa tttctaaaaa 60
atttaatgga ttcgttttct aaattcctga ttcgtcaaag gctgaagggc acgatagtaa 120
tagaaaatgg acggcagttt atcctttcat ggctggacac acagaatttg tggagggact 180
ctccattctg gtttatccgc cgttagttct ctctgtactc caccttagt tctctttgta 240
ctcgagacct ttaatgatta gccctgctta tgctgtcatt actgaactca cttccagagc 300
cccaaaaatc tct 313

<210> 42
<211> 713
<212> DNA
<213> Pinus radiata

<400> 42
taattcacaa gtagaaaatg agatttttgc aattttgtaa ctaacatttc ccggtctcct 60
ctgtatgttt tcacccctta atgtaattga aatttgcacc cgggttagat tcaaagcgga 120
gaataacatc ggggccttgt tctagacaga gatttttcac aaataacagg ttcgaaggta 180
tgtgtagaca tctgggtagt tgtagaataa agacggagcc cattaggtga tccaatcgaa 240
gagctcagat gggaaaacag ataaaaatta tcgggtggac cttccttcac atgttaatta 300
tatatcaagt gtcgccaatc cttatgtgaa acatttagta aagcttcgcc agagcacttc 360
ttataggcat tctgtgggct ctgttgttgt ggttggaagt actcctttaa gggaggtatc 420
tgaatatttg caacagaagt cagttaaaca agtggttgac tgtctgtttg tacaagatgt 480
tactggcata cctgtgggct tgatagagac ttccaggcgc attgtgcatg taaatcattt 540
ggtgatgcag aagctagccg gagtagagtc tatagagccc actgaagcaa ttggtgtaat 600
caagcttcct agcagcttct acaacttgga atctcttgaa attcactcta gttcccagat 660
atggtgctcg tcgccacatc gtctgcttgt acttgatggc attcaggatc ctg 713

<210> 43
<211> 28
<212> DNA
<213> Pinus radiata

<400> 43
ccacctcaca tcaataaatt ttatacga 28

<210> 44
<211> 35
<212> DNA
<213> Pinus radiata

<400> 44
gctgtttcat tggggtcata gctacgtggt gctga 35

<210> 45
<211> 1729

<212> DNA
<213> Pinus radiata

<400> 45
cttattgaca tataaaagca aagttggatc catctgttat tttgggtccc ctccagaagc 60
cttactaaat gcggacaaaa aatccacgta aagaacttct gaatttaccg tcatctgggc 120
tctgtaatta cgaatttagg gtttcctctg tcaatatctg gtagtgacaa acaaggttta 180
atggcagcct tagcaacaac tgaagtttgt gatacatatc cacgccttgt ggagaatggt 240
gagcttcgtg tcttgcaacc aattttccag atatatggtc gacgtcgagc tttctctgga 300
cctatagtta cactgaaggt ctttgaggac aatgtccttt tgcgggaatt ccttgaggag 360
agaggtaatg gaagagtttt ggtagttgat ggaggaggaa gccttagatg tgccatactg 420
gggggcaatg tagttgtatc tgcccaaaac aatggttggt ctggaataat tgtcactggc 480
tgcataaggg acgttgatga aataaacaga tgtgacattg gtataagagc actgacatct 540
aacccactga aggccaacaa gaagggtgtg ggtgaaaaac atgcgcctat ttacattgct 600
ggtacccgca ttcttccggg ggaatggtgt tatgctgaca gtgatggtat tcttgtttca 660
cagcaagagt tatcactgtg agataataaa attcataagt ttcagattgt gactttcatg 720
tcctgtggaa catatatttg actcgagtta gattctaata ggattaattg atagattctg 780
aaaattgagg aatatctctg gtcatgaaaa tcttcttctc atgtgatctt ttatgctcag 840
ctttgagtac aggatgataa gaagtttgtg catgtttgtc taaaggttta gcaagtatta 900
tcggaccatc ataagagata gattatggaa ctcagggact tgctatttt aatccaaaat 960
aacatttatt ctttgtgttt ttgccaaatt aacttttatt tcccttggca ccactagtga 1020
tttgcaatat ccagttgctg agaacataga agtgggcaac ggtgagagtt gcaacagtat 1080
ctagcataga tttaacaagt attgttggat cattataaga aaataaacta cagaaccaag 1140
ggaatctagt tgacaacata gttaaagtag gcatggtgct actgtatcga tacatcttca 1200
taaacagaaa aatatgaaca agctctaatg atgggagaaa ctccagcttg gtgttttgat 1260
taagcatcca tattcacacc taaaaggtta caagttccaa aataaaaatt ccaatgaatt 1320
tagccaatct aatcagacct tataagaaat acactaggca tctggggatc aaaatccagt 1380
agtttagaaa gtagttgtaa ataacccaga gacaaaaatc tcaatgatag cttgcttggg 1440
tcataggttt gataataatt gaaaacatag ttgaaaggag aatcctagca atggctagct 1500
tgaataatag atgtacagca aaattacagt agttgagaac aaagatggaa ggataatccc 1560
aacgatagct agcttggaca gtaggatgat tacatcaaaa tcatagcagt tgagaacata 1620
gttggaagga gaatccttat gatggctacg ttggataata ggcgtgatta tcgtaggtag 1680
attagagcac aagatcaaac taatagctgg cgcagctatc gactatttt 1729

<210> 46
<211> 1038
<212> DNA
<213> Pinus radiata

<400> 46
tgattactat agggcacgcg tggtcgacgg cccgggctgg taaatgagaa catgataagc 60
tgtgtaaatt catgctagtc accataactt ttctcattgc ttttcatcca cactgttgat 120
tcattcatta tataagatca gattcgtatg atatacaggc aaccatagaa acaaccagca 180
aagttactag caggaaatcc aactaggtat catgaagact accaacgcag gctcgataat 240
gttggtgctc attatttttg ggtgctgttt cattggggtc atagctacat cttttgattt 300
ctattacttc gttcaacagt ggcctggttc atactgcgat actcgtagag gatgctgtta 360
ccctcgcacg ggaaggcctg cttccgaatt ttccattcat ggcctctggc ccaactacaa 420
gaccggtaaa tggccacagt tctgtggttc ctccgaagaa ttcgactact caaagatctc 480
agatctggag gaggagctga acaggtattg gggttcgtta agctgtccaa gcagcgatgg 540
acaggaattt tggggacacg agtgggagaa acatggcact tgctctctca atcttgatga 600
gcattcatac tttgagaagg ctctctcctt gagacaaaat atagacattc ttggggctct 660
taaaactgca ggtattaaac ccgatggaag ccaatacagt ttgagcgata tcaaggaagc 720
cattaaacaa aacactgggc agctcccagg aatcgattgc aacacgagcg cagagggaga 780
gcatcaacta tatcaggtgt atgtgtgtgt tgataaatcc gatgcttcca ctgttattga 840
atgccccatt tatccacaca gcaattgccc atccatggtt gtgtttcctc cttttgggga 900
ggatcaggag gaccgagatg gttacacaga aggaatgtac gagctgtaga tctggacaaa 960
cagcatttct tctctccgca tttgattttt atcaatgaaa tttccgattc caacattttg 1020

taaaaaaaaa aaaaaaaa 1038

<210> 47
<211> 91
<212> DNA
<213> Pinus radiata

<400> 47
aattttccat tcatgcctct gcccaactac aagaccggta aatggccaca gttctgtggt 60
tcctccgaag aattcgatat caagcttatc g 91

<210> 48
<211> 91
<212> DNA
<213> Pinus radiata

<400> 48
gcttttcatc cacactggtg cctcattcat tatataagat cagattcgtg tgatatacag 60
gcaaccatag aaacaaccgg caaagttact a 91

<210> 49
<211> 809
<212> DNA
<213> Pinus radiata

<400> 49
tgatatatat aacttctagc agaatgacac gcgacttgta tatcttttca ttttttaacc 60
catgaaaacc gattagggta ttgcaaatta gggcattgcc attcaaataa ttctcagatg 120
aaagattctc tctaacaatt acaaatgatt atttttttcc atgagtgttg catgttcgaa 180
cggtctgccc agtctgtgag agagcataga gaaccctccc tgcccaattt gttagagcat 240
agagaaccct actgcatgag tagtaagaaa aatattcggt ctcaattcgg caaagaccac 300
ctcgaatgga tgacttcaac gacaatctca tgatagtgtt ctgatcagca ccagttcacc 360
tatatatttt atctagggtt tagtttgcat gtatcaatcc tctggtgcac taggtaattc 420
tttcccagta tcatatatcc ttaatactgt tttgtctttt aatccatggc taccatcaga 480
acaagctcaa agcagaataa gggagcatca gccatcctct tgcttatcgc gattgcaggg 540
ttagtaaatg cgtgcaacgc tgtgggtatt gagccaatgt gcgacactgt ggtgtcgagt 600
cttctgaggc ttctgccatg caggacggct gttgatccct caattgccgc cattccactt 660
ccaagctgct gcaacgcggt tgagtcagct gggcttcaat gcctctgtct cgtcgttaac 720
ggccctcctt ttccaggggt cgaccgcggc ctcgcaatgc agctgcctgc caaatgccat 780
ctcacccttc ctccctgtaa cagttagtt 809

<210> 50
<211> 428
<212> DNA
<213> Eucalyptus grandis

<400> 50
tttcttgtga ctattcattt tcctcctgat tatccattca agcccccgaa ggttgcattt 60
aggactaaag ttttccaccc aaatataaat aacaatggaa gtatctgcct tgacatcttg 120
aaggaacagt ggagtcctgc tttgacaatc tccaaggttt tgctctcaat ttgctctttg 180
ttgacggatc caaacccaga tgatcctctt gtaccagaga ttgctcatat gtacaagact 240
gataggggca aatatgagtc cactgcacgg agttggactc agaaatatgc aatgggttaa 300
ctttaaaaac tatatatcag tgatggaact ttatccctaa gttggaatct cttcgaatca 360
atgacttgtt tgcttgtaag aaatgtttcc ttaagataag tggctttcct caaaacttga 420
ttgaagtg 428

<210> 51

<211> 525
<212> DNA
<213> Pinus radiata

<400> 51
ccctttctttg ccttcaacta atcctgctca tcctctcctg cccccattcc caaagatggc 60
tgcacccaga tcatccgcta aattgggtgc acttttggca atactgctca tagttgcggc 120
agcgcaggct caagattgct caaatgccat ggacaaattg gctccatgca cttcagcagt 180
gggactgtct agcaatggag tgaagccctc atctgagtgc tgtgatgccc tcaaaggaac 240
cagtactggc tgcgtctgca agtctgtgag agcagtgata tcacttcctg ctaagtgcaa 300
tctcccagcc ataacctgct ctggatctcg ctgaaggctc tctgttatgg cgattctcag 360
atcgtggatc tctttaagat tttcagcaag caagtgatag aataaattct cagattttga 420
gatatctata tagcgatttt cagtatcaga ttgtctatag tactcatata tttaagtgat 480
tgaatagcat tctccgattc cgagttggaa acacagacac aatga 525

<210> 52
<211> 1126
<212> DNA
<213> Pinus radiata

<400> 52
actagtgatt actatagggc acgcgtggtc gacggcccgg gctggtaaat acccaactta 60
atttaattgt tattgagcca gagagatgcg tagtcgctca tgtcacttgt gtttaccaaa 120
aagacataca taaacacctg cacctaaaag ttataatgat aacatgcata caaccctaca 180
acgtacgtag tcacatgcgg ctagaactta aacccctacc acaaacatag ccacctgcac 240
ccagaagtta taataataac atacatagaa cccttacaat aaaaaaagtt atctccaatg 300
attattaatc tactgcaggc cagccatact cagcttgaac gtgaaaattc gcattgtaag 360
catggcgcca cattaaaata acctcggcaa tattttcatg tccaagtggc cggccagcca 420
cgctcctcgc actctgagaa tactctattc atccacttgt ctctgccccg caactcatat 480
aaatgtggcc aacccaagca ccatatccat gttcattaat cccctctttg ccttcaacta 540
atcctgctca tcgcctcttg ccccaattcc caaagatggc tgcacccaga tcatccgcta 600
aatcggctgc acttttcgca atactgctca tagttgcggc agtacaggct gaagattgct 660
caaatgccat ggacaaattg gctccatgca cttcagcagt gggactgtct agcaatggag 720
tgaagccctc atctgagtgc tgtgatgccc tcaaaggaac cagtactggc tgcgtctgca 780
aatctgtgag agcagtgata tcacttcctg ctaagtgcaa tctcccagcc ttaacctgct 840
ctggatctcg ctgaaggctc tctgttatgg cgattctcag atcgtggatc tctttaagat 900
tttcaggaag caagtgatag aataaattct cagatgttga gatatctata tagcgatttt 960
cagtatcaga ttgtctacag taccaatata tttaagtgat tgaatggaat tctcggattc 1020
tgagatagaa atataggcac agaatgtggc cggaggaatg ttcgaattcg agaatgataa 1080
taaataataa atgattgatt tctctctgca aaaaaaaaaa aaaaaa 1126

<210> 53
<211> 454
<212> DNA
<213> Pinus radiata

<400> 53
atcctgctca tcctctcctg cccccattcc caaagatggc tgcacccaga tcatccgcta 60
aattgggtgc acttttggca atactgctca tagttgcggc agcgcaggct caagattgct 120
caaatgccat ggacaaattg gctccatgca cttcagcagt gggactgtct agcaatggag 180
tgaagccctc atctgagtgc tgtgatgccc tcaaaggaac cagtactggc tgcgtctgca 240
agtctgtgag agcagtgata tcacttcctg ctaagtgcaa tctcccagcc ataacctgct 300
ctggatctcg ctgaaggctc tctgttatgg cgattctcag atcgtggata tctttaagat 360
tttcagcaag tgatagaata aattctcaga ttttgagata tctatatagc gattttcagt 420
atcagattgt ctatagtact catatattta agtg 454

<210> 54

<211> 335
<212> DNA
<213> Pinus radiata

<400> 54
agaagcacct gttaaaaagg aggcctgctc tttgttcatg agcttataga taagccctag 60
tctgcaagga ttattgccct gtagttattt ggaagtagat cattttcaca ggcccagatg 120
cattatattc taatgcagtt gtttgttaat tgaagtgcaa atagttccaa aatgtttaca 180
tgaatcaata gtgaacaaat ccctctgttt tatatcatat tgatggatta ttcgattttt 240
tggtgacgtg gcgcgaaact gcttttcgaa ctcatggaaa tagtaattgt tataatccat 300
aggcatgaga ttcttgttaa tcgtgcacaa ggttt 335

<210> 55
<211> 336
<212> DNA
<213> Pinus radiata

<400> 55
aaaccttgtg cacgattaac aagaatctca tgcctatgga ttataacaat tactatttcc 60
atgagttcga aaagcagttt cgcgccacgt caccaaaaaa tcgaataatc catcaatatg 120
atataaaaca gagggatttg ttcactattg attcatgtaa acattttgga actatttgca 180
cttcaattaa caaacaactg cattagaata taatgcatct ggtgcctgtg aaaatgatct 240
acttccaaat aactacaggg caataatcct tgcagactag ggcttatcta taagctcatg 300
aacaaagagc aggcctcctt tttaacaggt gcttct 336

<210> 56
<211> 532
<212> DNA
<213> Pinus radiata

<400> 56
cgttcgttcc cttccctttc cattgttgcg tttaagccct ccaattttct tttggcgtcc 60
cgtttttggg gctcccttga agatctcctc ttcatttcgg gatttcctgc cttcgccgcg 120
ccatttgaag ttctttttct gagagaagaa tttagacatg gctgatcgca tgttgactcg 180
aagccacagc cttcgcgagc gtttggacga gaccctctct gctcaccgca acgatattgt 240
ggccttcctt tcaagggttg aagccaaggg caaaggcatc ttgcagcgcc accagatttt 300
tgctgagttt gaggccatct ctgaggagag cagagcaaag cttcttgatg gggcctttgg 360
tgaagtcctc aaatccactc aggaagcgat tgtgtcgcct ccatgggttg ctcttgctgt 420
tcgtccaagg ccgggcgtgt gggagcacat ccgtgtgaac gtccatgcgc ttgttcttga 480
gcaattggag gttgctgagt atctgcactt caaagaagag cttgctgatg ga 532

<210> 57
<211> 3103
<212> DNA
<213> Eucalyptus grandis

<400> 57
gggtgaaaac aattaatgag atcatttgaa ttaaggaaag tggaaaggcg gttttctgat 60
tggtacactg aaacaacagg aaggtggtgg aggccgcaat gatggaattt atccacttta 120
atcattttat gaaatcgata cactaacctt tgtttctcct aaacccaaag gcattaatcc 180
ctgtcctcct cactcgatct cgaaggccag aaggggggagg ccgagcctct tgcttttttt 240
cgtgtataaa agggcctccc ccattcctca tttttcacca tcctccgttc gttcgttccc 300
ttccctttcc attgttgcgt ttaagccctc caattttctt ttggcgtccc gtttttgggg 360
ctcccttgaa gatctcctct tcatttcggg atttcctgcc ttcgccgcgc catttgaagt 420
tcttttttctg agagaagaat ttagacatgg ctgatcgcat gttgactcga agccacagcc 480
ttcgcgagcg tttggacgag accctctctg ctcaccgcaa cgatattgtg gccttccttt 540
caagggttga agccaagggc aaaggcatct tgcagcgcca ccagattttt gctgagtttg 600

aggccatctc tgaggagagc agagcaaagc ttcttgatgg ggcctttggt gaagtcctca 660
aatccactca ggaagcgatt gtgtcgcctc catgggttgc tcttgctgtt cgtccaaggc 720
cgggcgtgtg ggagcacatc cgtgtgaacg tccatgcgct tgttcttgag caattggagg 780
ttgctgagta tctgcacttc aaagaagagc ttgctgatgg aagcttgaat ggtaactttg 840
tgcttgagct tgactttgag ccattcactg cctcttttcc gcgcccgact ctttccaagt 900
ctattggcaa tggcgtcgag tttctcaatc gccatctctc cgctaagctc ttccatgaca 960
aggaaagctt gcaccctctg cttgaattcc tccaagtcca ctgctacaag gggaagaaca 1020
tgatggtgaa tgccagaatc cagaatgtgt tctccctcca acatgtcctg aggaaggcgg 1080
aggagtatct gacctcgctc aaacccgaga ccccgtactc ccagttcgag cacaagttcc 1140
aggagatcgg gctcgagcgg gggtggggtg acacggctga gcgcgtcctc gagatgatcc 1200
agctcctgtt ggatctcctt gaggctcccg acccgtgcac tctcgagaag ttcttggata 1260
gggttcccat ggtcttcaac gtcgtgatca tgtctcccca cggatacttt gctcaggacg 1320
acgtccttgg ttatccggat accggtggcc aggttgttta catcctggat caagttcgtg 1380
ccctagagga agaaatgctt caccgcatta agcaacaagg actggatatt actcctcgga 1440
ttctcattat cactcggctt cttccagacg cggttggaac cacctgtggc cagcgccttg 1500
agaaagtttt tgggaccgag tactcccaca ttcttcgcgt cccttcaga aatgagaagg 1560
gagtcgtccg caagtggatt tcccggttcg aggtgtggcc ctatttggaa agatacactg 1620
aggatgtcgc gagcgaactt gctggagagt tgcagggcaa gcctgatctg atcatcggaa 1680
actacagtga tggaaacatt gttgcttcct tgttagcaca taaattaggt gttacacagt 1740
gtacaatagc ccatgccctc gagaagacga agtacccaga gtcagacata tactggaaga 1800
aatttgagga aaagtaccac ttctcttgcc agttcactgc tgatctcatc gccatgaacc 1860
acaccgactt cattatcacc agcaccttcc aagaaattgc tggaagcaag gatacagtgg 1920
ggcagtatga gagtcacatg aacttcactc ttcctggact ctaccgagtt gtccacggga 1980
tcgacgtctt cgacccgaag ttcaacattg tttcaccagg tgctgacatg agcatctact 2040
ttgcttacac cgaacaggag cggcggttga aatccttcca ccctgagatc gaggaactcc 2100
tcttcagcga tgttgagaac aaggaacact tgtgtgtgtt gaaagataag aagaagccta 2160
ttattttcac catggcaagg ctggaccgtg tcaagaactt gacagggctt gttgagtggt 2220
atggcaagaa ctccaagttg agggaactcg ccaacttggt cgtggttgga ggtgacagga 2280
ggaaggattc gaaggacttg gaagagcagt ctgagatgaa gaaaatgtac gacctcatcg 2340
aaaagtacaa gctgaatggc cagttcaggt ggatttcctc ccagatgaac cgggtgagga 2400
atggagagct ctaccgctac atctgtgaca cgaagggagt cttcgttcaa ccggctatct 2460
atgaagcttt cgggttgacc gtggttgagg ccatgacttg tggattgcca acctttgcca 2520
cttgcaatgg tggaccagct gagatcattg tgcatggcaa atcgggctac cacattgatc 2580
cttaccatgg tgaccaggcg gccgagcttc ttgtagactt cttcaacaag tgcaagattg 2640
accagtccca ctgggacgag atctcaaagg gtgccatgca gagaattgaa gagaagtata 2700
catggaaaat atattctgag aggctgttga acctgactgc cgtgtatggc ttctggaagc 2760
atgtgactaa ccttgatcgg cgcgagagtc gccggtacct tgaaatgttc tatgccctca 2820
agtatcgccc actggcacag tctgttcctc cggctgtcga gtaaacaaag agacagattg 2880
ttaccagaag acggaagcat tggacttttg aagttttcaa ggaataaaca ttggaaattg 2940
tttgaatttg ggattgccaa gagcgatctt tttcgtttcc ttttttggt ccttttctc 3000
ttctttgttt ccattccgcg aatgtttgca ttttggggtt tgtacccatc aattcagtaa 3060
atggttcatt ttcttttcaa aaaaaaaaaa aaaaaaaaaa aaa 3103

<210> 58
<211> 326
<212> DNA
<213> Eucalyptus grandis

<400> 58
ctcgaaaccg agacgctgac tgtgggttga gctctaacca atgggagtga tgtctctctt 60
acgtgcctgc cgtgggcccc agtgacgggc cccaaaagtg taaacgaagg aagctcccgg 120
ggatctgatt ggccgcgacg tccgcctctg acgtggcacc accgacgatt ttttttaat 180
atcttggtca agtcctaatt taactatggg gtccagatta gaagcttatc cactatggat 240
taaattaaat caaatgggaa ttaaattaaa ttaaaatcat cgtgcggagg tgcacgagat 300
gcacgagatc cgacggcgca gagcag 326

<210> 59

<211> 311
<212> DNA
<213> Eucalyptus grandis

<400> 59
attactatag ggcacgcgtg gtcgacggcc cgggctggta ctctcactaa ttctttagtt 60
ttccaattta gccccttctg taattgctca tcttctttac caaattctct aatttggccg 120
gcgaagggct gacaagggat tggtcatgtc accctcacca aaggttgccg aaggtccggt 180
gacctcagct gacggccacc tacaccaaat ctagctcact agcagcctaa gcccttcatc 240
aactctagtg aaaggttttg agtatttttt aataaaaaat atttaaaaaa tatatagcga 300
gagctcatta c 311

<210> 60
<211> 2096
<212> DNA
<213> Eucalyptus grandis

<400> 60
gattactata gggcacgcgt ggtcgacggc ccgggctggt ctgagccatt taattcgaga 60
gcacatcgcc caaaattatt cttcttgctg ccataactgt cgaattttct cttttaggta 120
agtaaccaat gatgcatcat gttgacaaaa aggctgatta gtatgatctt ggagttgttg 180
gtgcaaattt gcaagctgac gatggccccc cagggaaatt aaggcgccaa cccagattgc 240
aaagagcaca aagagcacga tccaaccttt ccttaacaag atcatcacca gatcggccag 300
taagggtaat attaatttaa caaatagctc ttgtaccggg aactccgtat ttctctcact 360
tccataaacc cctgattaat ttggtgggaa agcgacagcc aacccacaaa aggtcagatg 420
tcatcccacg agagagagag agagagagag agagagagag agagttttct ctctatattc 480
tggttcaccg gttggagtca atggcatgcg tgacgaatgt acatattggt gtagggtcca 540
atattttgcg ggagggttgg tgaaccgcaa agttcctata tatcgaacct ccaccaccat 600
acctcacttc aatccccacc atttatccgt tttatttcct ctgctttcct ttgctcgagt 660
ctcgcggaag agagagaaga gaggagagga gagaatgggt tcgaccggat ccgagaccca 720
gatgaccccg acocaagtct cggacgagga ggcgaacctc ttcgccatgc agctggcgag 780
cgcctccgtg ctccccatgg tcctcaaggc cgccatcgag ctcgacctcc tcgagatcat 840
ggccaaggcc gggccgggcg cgttcctctc cccgggggaa gtcgcggccc agctcccgac 900
ccagaacccc gaggcacccg tcatgctcga ccggatcttc cggctgctgg ccagctactc 960
cgtgctcacg tgcaccctcc gcgacctccc cgatggcaag gtcgagcggc tctacggctt 1020
agcgccggtg tgcaagttct tggtcaagaa cgaggacggg gtctccatcg ccgcactcaa 1080
cttgatgaac caggacaaaa tcctcatgga aagctggtat tacctgaaag atgcggtcct 1140
tgaaggcgga atcccattca acaaggcgta cgggatgacc gcgttcgagt atcatggcac 1200
cgacccgcga ttcaacaaga tctttaaccg gggaatgtct gatcactcca ccattactat 1260
gaagaagata ctggaaacat acaagggctt cgagggcctc gagaccgtgg tcgatgtcgg 1320
aggcggcact ggggccgtgc tcagcatgat cgttgccaaa tacccatcaa tgaaagggat 1380
caacttcgac cgccccaacg gattgaagac gccccacccc ttcctggtgt caagcacgtc 1440
ggaggcgaca tgttcgtcag cgttccaaag ggagatgcca ttttcatgaa gtggatatgc 1500
catgactgga gtgacgacca ttgcgcgaag ttcctcaaga actgctacga tgcgcttccc 1560
aacaatggaa aggtgatcgt tgcagagtgc gtactccctg tgtacccaga cacgagccta 1620
gcgaccaaga atgtgatcca catcgactgc atcatgttgg cccacaaccc aggcgggaaa 1680
gagaggacac agaaggagtt cgaggcattg gccaaagggg ccggatttca gggcttccaa 1740
gtcatgtgct gcgctttcgg cactcacgtc atggagttcc tgaagaccgc ttgatctgct 1800
cctctgtggt gatgttcatg gttcttggat ttgaaaggtc gtgaaggagc ccttttctca 1860
cagttggctt cggcatacca agttcttctc ataaaaggaa acaataagaa gcgactgtat 1920
gatggcgcaa gtggaagtta caagatttgt tgttttatgt ctataaagtt ttgagtcttc 1980
tgcatactga tttcacagaa tgtgtaacga aacggcgtat atggatgtgc ctgaatgatg 2040
gaaattgtga tattctgtct tctttttcag taaatcactt cgaacaaaaa aaaaaa 2096

<210> 61
<211> 522
<212> DNA

<213> Eucalyptus grandis

<400> 61
ctaaaacgct aatcctgccc tgcccttccc ttctgctgct gctgctcgtc acctctctct 60
ccctctcgcg gccagctgcg agatctgccg agtttaagcc tcgtacatca aaatgggtaa 120
ggagaagatt cacatcagca ttgtggtcat tggccatgtc gattctggga agtcaaccac 180
aactggccac ttgatataca agctcggagg aatcgacaag cgtgtgattg agagattcga 240
gaaggaagct gctgagatga acaagagatc gttcaagtat gcttgggtgc ttgacaagct 300
caaggccgag cgcgagcgcg gtattaccat tgatattgcc ttgtggaagt tcgagaccac 360
caagtactac tgcactgtca ttgatgctcc tggacatcgt gactttatta agaatatgat 420
tactggaacc tcccaggccg actgtgctgt ccttatcatt gattccacca ctggtggttt 480
cgaagctggt atttccaagg atggccagac ccgtgaacat gc 522

<210> 62
<211> 420
<212> DNA
<213> Eucalyptus grandis

<400> 62
tttgatacgc taacaaacaa aacatgtgaa aagcttaatt atggcaatta tcataaatag 60
aaaaaaatta gaaaaaaaga gaggaaatgg gccattattt aaattgcaat cgaaagattg 120
agggcaattc tgtttctcta gtgtaaataa gggtgtattt aataattgag ggatggaaat 180
agcatggtca ctcggtaatt atcaaggaaa gcaagaataa aaatggaaaa aaaaaaaaaa 240
aaagcttgaa gaggccaatg tcgaaattat gagcgcgaga tgaggacact cctgggaaac 300
gaaaaatggc attcgcgggg ggtgctatat aaagcctcgt gtaagggtgc gttcctcact 360
ctcaaaccct aatcctgccc ttcccttctg ctgctgctgc tcgtcacctc tctcctccct 420

<210> 63
<211> 65
<212> PRT
<213> Eucalyptus grandis

<400> 63
Met Asp Asn Ser Lys Met Gly Phe Asn Ala Gly Gln Ala Lys Gly Gln
1 5 10 15
Thr Gln Glu Lys Ser Asn Gln Met Met Asp Lys Ala Ser Asn Thr Ala
20 25 30
Gln Ser Ala Arg Asp Ser Met Gln Glu Thr Gly Gln Gln Met Lys Ala
35 40 45
Lys Ala Gln Gly Ala Ala Asp Ala Val Lys Asn Ala Thr Gly Met Asn
50 55 60
Lys
65

<210> 64
<211> 152
<212> PRT
<213> Eucalyptus grandis

<400> 64
Met Gly Gly Pro Leu Thr Leu Asp Ala Glu Val Glu Val Lys Ser Pro
1 5 10 15
Ala Asp Lys Phe Trp Val Ser Val Arg Asp Ser Thr Lys Leu Phe Pro
20 25 30
Lys Ile Phe Pro Asp Gln Tyr Lys Asn Ile Glu Val Leu Glu Gly Asp
35 40 45
Gly Lys Ala Pro Gly Ser Val Arg Leu Phe Thr Tyr Gly Glu Gly Ser

```
    50                  55                  60
Pro Leu Val Lys Val Ser Lys Glu Lys Ile Asp Gly Val Asp Glu Ala
65                  70                  75                  80
Asp Lys Val Val Thr Tyr Ser Val Ile Asp Gly Asp Leu Leu Lys Tyr
                85                  90                  95
Tyr Lys Asn Phe Asn Gly Ser Ile Lys Val Ile Pro Lys Gly Asp Gly
            100                 105                 110
Ser Leu Val Lys Trp Ser Cys Gly Phe Glu Lys Ala Ser Asp Glu Ile
        115                 120                 125
Pro Asp Pro His Val Ile Lys Asp Phe Ala Ile Gln Asn Phe Lys Glu
    130                 135                 140
Leu Asp Glu Phe Ile Leu Lys Ala
145                 150
```

<210> 65
<211> 117
<212> PRT
<213> Eucalyptus grandis

<400> 65

```
Met Ala Ala Asn Phe Val Ile Pro Thr Lys Met Lys Ala Trp Val Tyr
 1               5                  10                  15
Arg Glu His Gly Asn Val Ala Asp Val Leu Gly Leu Asp Pro Glu Leu
            20                  25                  30
Lys Val Pro Glu Leu Gln Glu Gly Gln Val Leu Val Lys Val Leu Ala
        35                  40                  45
Ala Ala Leu Asn Pro Val Asp Ala Ala Arg Met Lys Gly Val Ile Lys
    50                  55                  60
Leu Pro Gly Phe Ser Leu Pro Ala Val Pro Gly Tyr Asp Leu Ala Gly
65                  70                  75                  80
Val Val Val Lys Val Gly Arg Glu Val Lys Glu Leu Lys Ile Gly Asp
                85                  90                  95
Glu Val Tyr Gly Phe Met Phe His Ala Lys Lys Asp Gly Thr Leu Ala
            100                 105                 110
Glu Tyr Ala Ala Val
        115
```

<210> 66
<211> 318
<212> PRT
<213> Eucalyptus grandis

<400> 66

```
Met Ala Ala Asn Phe Val Ile Pro Thr Lys Met Lys Ala Trp Val Tyr
 1               5                  10                  15
Arg Glu His Gly Asp Val Ala Asn Val Leu Gly Leu Asp Pro Glu Leu
            20                  25                  30
Lys Val Pro Glu Leu Gln Glu Gly Gln Val Leu Val Lys Val Leu Ala
        35                  40                  45
Ala Ala Leu Asn Pro Ile Asp Thr Ala Arg Val Lys Gly Val Ile Lys
    50                  55                  60
Leu Pro Gly Phe Ser Leu Pro Ala Val Pro Gly Tyr Asp Leu Ala Gly
65                  70                  75                  80
Val Val Val Lys Val Gly Arg Glu Val Lys Glu Leu Lys Val Gly Asp
                85                  90                  95
Glu Val Tyr Gly Phe Met Phe His Ala Lys Lys Asp Gly Thr Leu Ala
            100                 105                 110
```

```
Glu Tyr Ala Ala Val Glu Glu Ser Phe Leu Ala Leu Lys Pro Lys Lys
        115                 120                 125
Leu Arg Phe Gly Glu Ala Ala Ser Leu Pro Val Val Ile Gln Thr Ala
    130                 135                 140
Tyr Gly Gly Leu Glu Arg Ala Gly Leu Ser His Gly Lys Ser Leu Leu
145                 150                 155                 160
Val Leu Gly Gly Ala Gly Gly Val Gly Thr Leu Ile Ile Gln Leu Ala
                165                 170                 175
Lys Glu Val Phe Gly Ala Ser Arg Val Ala Ala Thr Ser Ser Thr Gly
            180                 185                 190
Lys Leu Glu Leu Leu Lys Ser Leu Gly Ala Asp Leu Ala Ile Asp Tyr
        195                 200                 205
Thr Lys Val Asn Phe Glu Asp Leu Pro Glu Lys Phe Asp Val Val Tyr
    210                 215                 220
Asp Thr Val Gly Glu Ile Glu Arg Ala Ala Lys Ala Val Lys Pro Gly
225                 230                 235                 240
Gly Ser Ile Val Thr Ile Val Lys Gln Asn Lys Thr Leu Pro Pro Pro
                245                 250                 255
Ala Phe Phe Phe Ala Val Thr Ser Asn Arg Ser Thr Leu Glu Lys Leu
            260                 265                 270
Lys Pro Phe Leu Glu Ser Gly Lys Val Lys Pro Val Ile Asp Pro Lys
        275                 280                 285
Ser Pro Phe Pro Phe Ser Gln Ala Ile Glu Ala Phe Ser Tyr Leu Gln
    290                 295                 300
Thr Arg Arg Ala Thr Gly Lys Leu Val Ile His Pro Val Pro
305                 310                 315
```

<210> 67
<211> 156
<212> PRT
<213> Eucalyptus grandis

<400> 67

```
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
 1               5                  10                  15
Val Glu Ser Ser Asp Thr Val Asp Asn Val Lys Ala Lys Ile Gln Asp
            20                  25                  30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
        35                  40                  45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
    50                  55                  60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65                  70                  75                  80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
                85                  90                  95
Asp Thr Val Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
            100                 105                 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
        115                 120                 125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
    130                 135                 140
Leu Val Leu Arg Leu Lys Gly Gly Met Gln Ile Phe
145                 150                 155
```

<210> 68
<211> 238
<212> PRT

<213> Eucalyptus grandis

<400> 68

```
Met Ala Thr His Ala Ala Leu Ala Pro Ser Thr Leu Pro Ala Asn Ala
 1               5                  10                  15
Lys Phe Ser Ser Lys Ser Ser Ser His Ser Phe Pro Thr Gln Cys Phe
            20                  25                  30
Ser Lys Arg Leu Glu Val Ala Glu Phe Ser Gly Leu Arg Ala Gly Ser
        35                  40                  45
Cys Val Thr Tyr Ala Lys Asn Ala Gly Glu Gly Ser Phe Phe Asp Ala
    50                  55                  60
Val Ala Ala Gln Leu Thr Pro Lys Thr Ser Ala Pro Ala Pro Ala Lys
65                  70                  75                  80
Gly Glu Thr Val Ala Lys Leu Lys Val Ala Ile Asn Gly Phe Gly Arg
                85                  90                  95
Ile Gly Arg Asn Phe Leu Arg Cys Trp His Gly Arg Lys Asn Ser Pro
            100                 105                 110
Leu Asp Val Ile Val Val Asn Asp Ser Gly Gly Val Lys Asn Ala Ser
        115                 120                 125
His Leu Leu Lys Tyr Asp Ser Met Leu Gly Thr Phe Lys Ala Asp Val
    130                 135                 140
Lys Ile Val Asp Asn Glu Thr Ile Ser Val Asp Gly Lys Pro Val Lys
145                 150                 155                 160
Val Val Ser Asn Arg Asp Pro Leu Lys Leu Pro Trp Ala Glu Leu Gly
                165                 170                 175
Ile Asp Ile Val Ile Glu Gly Thr Gly Val Phe Val Asp Gly Pro Gly
            180                 185                 190
Ala Gly Lys His Ile Gln Ala Gly Ala Lys Lys Val Ile Ile Thr Ala
        195                 200                 205
Pro Ala Lys Gly Ala Asp Ile Pro Thr Tyr Val Tyr Gly Val Asn Glu
    210                 215                 220
Thr Asp Tyr Ser His Glu Val Ala Asn Ile Ile Ser Asn Ala
225                 230                 235
```

<210> 69
<211> 168
<212> PRT
<213> Eucalyptus grandis

<400> 69

```
Met Ser Thr Ser Pro Val Ser Ser Trp Cys Ala Thr Ser Phe Ser Pro
 1               5                  10                  15
Ala His Ser Ser Leu Lys Arg Ala Ala Gly Leu Arg Pro Ser Leu Ser
            20                  25                  30
Ala Arg Leu Gly Pro Ser Ser Ser Ser Ser Ser Val Ser Pro Pro Thr
        35                  40                  45
Leu Ile Arg Asn Glu Pro Val Phe Ala Ala Pro Ala Pro Val Ile Asn
    50                  55                  60
Pro Thr Trp Thr Glu Glu Met Gly Lys Asp Tyr Asp Glu Ala Ile Glu
65                  70                  75                  80
Ala Leu Lys Lys Leu Leu Ser Glu Lys Gly Asp Leu Lys Ala Thr Ala
                85                  90                  95
Ala Ala Lys Val Glu Gln Ile Thr Ala Glu Leu Gln Thr Ala Ser Pro
            100                 105                 110
Asp Ile Lys Pro Ser Ser Ser Val Asp Arg Ile Lys Thr Gly Phe Thr
        115                 120                 125
Phe Phe Lys Lys Glu Lys Tyr Asp Lys Asn Pro Ala Leu Tyr Gly Glu
```

130 135 140
Leu Ala Lys Gln Ser Pro Lys Phe Met Val Phe Ala Cys Ser Asp Ser
145 150 155 160
Arg Val Cys Pro Ser His Val Leu
165

<210> 70
<211> 214
<212> PRT
<213> Eucalyptus grandis

<400> 70
Met Pro Cys Pro Arg Ala Pro Pro Met Met Glu Arg Arg Ile Lys Pro
1 5 10 15
Gln Thr Glu Gln Ala Leu Lys Cys Pro Arg Cys Asp Ser Thr Asn Thr
20 25 30
Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Leu Ser Gln Pro Arg His Phe
35 40 45
Cys Lys Thr Cys Arg Arg Tyr Trp Thr Lys Gly Gly Ala Leu Arg Asn
50 55 60
Val Pro Val Gly Gly Gly Cys Arg Lys Asn Lys Arg Ala Lys Arg Ala
65 70 75 80
Val Asp His Pro Val Ser Ala Gln Asn Glu Ala Ser Thr Ser Ala Ala
85 90 95
Pro Gly Asn Glu Val Pro Asp Arg Ser Pro Phe Glu Pro Pro Ser Ser
100 105 110
Lys Ser Ile Tyr Tyr Gly Gly Glu Asn Met Asn Leu Thr Gly Leu Pro
115 120 125
Phe Ser Arg Ile Gln Gln Asp Arg Ala Ala Leu Ala His Cys Asn Ser
130 135 140
Ser Ser Phe Leu Gly Met Ser Cys Gly Thr Gln Ser Ala Ser Leu Glu
145 150 155 160
Pro His Leu Ser Ala Leu Asn Thr Phe Asn Ser Phe Lys Ser Asn Asn
165 170 175
Pro Gly Leu Asp Phe Pro Ser Leu Ser Thr Asp Gln Asn Ser Leu Phe
180 185 190
Glu Thr Ser Gln Pro Gln Leu Ser Arg Ala Met Ala Ser Ala Leu Phe
195 200 205
Ser Met Pro Met Ala Pro
210

<210> 71
<211> 166
<212> PRT
<213> Pinus radiata

<400> 71
Met Ala Ala Leu Ala Thr Thr Glu Val Cys Asp Thr Tyr Pro Arg Leu
1 5 10 15
Val Glu Asn Gly Glu Leu Arg Val Leu Gln Pro Ile Phe Gln Ile Tyr
20 25 30
Gly Arg Arg Arg Ala Phe Ser Gly Pro Ile Val Thr Leu Lys Val Phe
35 40 45
Glu Asp Asn Val Leu Leu Arg Glu Phe Leu Glu Glu Arg Gly Asn Gly
50 55 60
Arg Val Leu Val Val Asp Gly Gly Gly Ser Leu Arg Cys Ala Ile Leu
65 70 75 80

```
Gly Gly Asn Val Val Val Ser Ala Gln Asn Asn Gly Trp Ser Gly Ile
                85                  90                  95
Ile Val Thr Gly Cys Ile Arg Asp Val Asp Glu Ile Asn Arg Cys Asp
            100                 105                 110
Ile Gly Ile Arg Ala Leu Thr Ser Asn Pro Leu Lys Ala Asn Lys Lys
        115                 120                 125
Gly Val Gly Glu Lys His Ala Pro Ile Tyr Ile Ala Gly Thr Arg Ile
    130                 135                 140
Leu Pro Gly Glu Trp Cys Tyr Ala Asp Ser Asp Gly Ile Leu Val Ser
145                 150                 155                 160
Gln Gln Glu Leu Ser Leu
                165
```

<210> 72
<211> 236
<212> PRT
<213> Pinus radiata

```
<400> 72
Met Leu Val Leu Ile Ile Phe Gly Cys Cys Phe Ile Gly Val Ile Ala
 1               5                  10                  15
Thr Ser Phe Asp Phe Tyr Tyr Phe Val Gln Gln Trp Pro Gly Ser Tyr
            20                  25                  30
Cys Asp Thr Arg Arg Gly Cys Cys Tyr Pro Arg Thr Gly Arg Pro Ala
        35                  40                  45
Ser Glu Phe Ser Ile His Gly Leu Trp Pro Asn Tyr Lys Thr Gly Lys
    50                  55                  60
Trp Pro Gln Phe Cys Gly Ser Ser Glu Glu Phe Asp Tyr Ser Lys Ile
65                  70                  75                  80
Ser Asp Leu Glu Glu Glu Leu Asn Arg Tyr Trp Gly Ser Leu Ser Cys
                85                  90                  95
Pro Ser Ser Asp Gly Gln Glu Phe Trp Gly His Glu Trp Glu Lys His
            100                 105                 110
Gly Thr Cys Ser Leu Asn Leu Asp Glu His Ser Tyr Phe Glu Lys Ala
        115                 120                 125
Leu Ser Leu Arg Gln Asn Ile Asp Ile Leu Gly Ala Leu Lys Thr Ala
    130                 135                 140
Gly Ile Lys Pro Asp Gly Ser Gln Tyr Ser Leu Ser Asp Ile Lys Glu
145                 150                 155                 160
Ala Ile Lys Gln Asn Thr Gly Gln Leu Pro Gly Ile Asp Cys Asn Thr
                165                 170                 175
Ser Ala Glu Gly Glu His Gln Leu Tyr Gln Val Tyr Val Cys Val Asp
            180                 185                 190
Lys Ser Asp Ala Ser Thr Val Ile Glu Cys Pro Ile Tyr Pro His Ser
        195                 200                 205
Asn Cys Pro Ser Met Val Val Phe Pro Pro Phe Gly Glu Asp Gln Glu
    210                 215                 220
Asp Arg Asp Gly Tyr Thr Glu Gly Met Tyr Glu Leu
225                 230                 235
```

<210> 73
<211> 92
<212> PRT
<213> Pinus radiata

```
<400> 73
Met Ala Ala Pro Arg Ser Ser Ala Lys Leu Gly Ala Leu Leu Ala Ile
```

```
 1               5                  10                  15
Leu Leu Ile Val Ala Ala Ala Gln Ala Gln Asp Cys Ser Asn Ala Met
            20                  25                  30
Asp Lys Leu Ala Pro Cys Thr Ser Ala Val Gly Leu Ser Ser Asn Gly
        35                  40                  45
Val Lys Pro Ser Ser Glu Cys Cys Asp Ala Leu Lys Gly Thr Ser Thr
    50                  55                  60
Gly Cys Val Cys Lys Ser Val Arg Ala Val Ile Ser Leu Pro Ala Lys
65                  70                  75                  80
Cys Asn Leu Pro Ala Ile Thr Cys Ser Gly Ser Arg
                85                  90
```

<210> 74
<211> 92
<212> PRT
<213> Pinus radiata

<400> 74

```
Met Ala Ala Pro Arg Ser Ser Ala Lys Ser Ala Ala Leu Phe Ala Ile
 1               5                  10                  15
Leu Leu Ile Val Ala Ala Val Gln Ala Glu Asp Cys Ser Asn Ala Met
            20                  25                  30
Asp Lys Leu Ala Pro Cys Thr Ser Ala Val Gly Leu Ser Ser Asn Gly
        35                  40                  45
Val Lys Pro Ser Ser Glu Cys Cys Asp Ala Leu Lys Gly Thr Ser Thr
    50                  55                  60
Gly Cys Val Cys Lys Ser Val Arg Ala Val Ile Ser Leu Pro Ala Lys
65                  70                  75                  80
Cys Asn Leu Pro Ala Leu Thr Cys Ser Gly Ser Arg
                85                  90
```

<210> 75
<211> 92
<212> PRT
<213> Pinus radiata

<400> 75

```
Met Ala Ala Pro Arg Ser Ser Ala Lys Leu Gly Ala Leu Leu Ala Ile
 1               5                  10                  15
Leu Leu Ile Val Ala Ala Ala Gln Ala Gln Asp Cys Ser Asn Ala Met
            20                  25                  30
Asp Lys Leu Ala Pro Cys Thr Ser Ala Val Gly Leu Ser Ser Asn Gly
        35                  40                  45
Val Lys Pro Ser Ser Glu Cys Cys Asp Ala Leu Lys Gly Thr Ser Thr
    50                  55                  60
Gly Cys Val Cys Lys Ser Val Arg Ala Val Ile Ser Leu Pro Ala Lys
65                  70                  75                  80
Cys Asn Leu Pro Ala Ile Thr Cys Ser Gly Ser Arg
                85                  90
```

<210> 76
<211> 125
<212> PRT
<213> Eucalyptus grandis

<400> 76

```
Met Ala Asp Arg Met Leu Thr Arg Ser His Ser Leu Arg Glu Arg Leu
```

```
 1               5                  10                  15
Asp Glu Thr Leu Ser Ala His Arg Asn Asp Ile Val Ala Phe Leu Ser
            20                  25                  30
Arg Val Glu Ala Lys Gly Lys Gly Ile Leu Gln Arg His Gln Ile Phe
        35                  40                  45
Ala Glu Phe Glu Ala Ile Ser Glu Glu Ser Arg Ala Lys Leu Leu Asp
    50                  55                  60
Gly Ala Phe Gly Glu Val Leu Lys Ser Thr Gln Glu Ala Ile Val Ser
65                  70                  75                  80
Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
                85                  90                  95
His Ile Arg Val Asn Val His Ala Leu Val Leu Glu Gln Leu Glu Val
            100                 105                 110
Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Ala Asp Gly
        115                 120                 125
```

<210> 77
<211> 805
<212> PRT
<213> Eucalyptus grandis

<400> 77

```
Met Ala Asp Arg Met Leu Thr Arg Ser His Ser Leu Arg Glu Arg Leu
 1               5                  10                  15
Asp Glu Thr Leu Ser Ala His Arg Asn Asp Ile Val Ala Phe Leu Ser
            20                  25                  30
Arg Val Glu Ala Lys Gly Lys Gly Ile Leu Gln Arg His Gln Ile Phe
        35                  40                  45
Ala Glu Phe Glu Ala Ile Ser Glu Glu Ser Arg Ala Lys Leu Leu Asp
    50                  55                  60
Gly Ala Phe Gly Glu Val Leu Lys Ser Thr Gln Glu Ala Ile Val Ser
65                  70                  75                  80
Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
                85                  90                  95
His Ile Arg Val Asn Val His Ala Leu Val Leu Glu Gln Leu Glu Val
            100                 105                 110
Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Ala Asp Gly Ser Leu Asn
        115                 120                 125
Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Thr Ala Ser Phe
    130                 135                 140
Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu
145                 150                 155                 160
Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Leu His
                165                 170                 175
Pro Leu Leu Glu Phe Leu Gln Val His Cys Tyr Lys Gly Lys Asn Met
            180                 185                 190
Met Val Asn Ala Arg Ile Gln Asn Val Phe Ser Leu Gln His Val Leu
        195                 200                 205
Arg Lys Ala Glu Glu Tyr Leu Thr Ser Leu Lys Pro Glu Thr Pro Tyr
    210                 215                 220
Ser Gln Phe Glu His Lys Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
225                 230                 235                 240
Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp
                245                 250                 255
Leu Leu Glu Ala Pro Asp Pro Cys Thr Leu Glu Lys Phe Leu Asp Arg
            260                 265                 270
Val Pro Met Val Phe Asn Val Val Ile Met Ser Pro His Gly Tyr Phe
```

```
        275                 280                 285
Ala Gln Asp Asp Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
    290                 295                 300
Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Glu Glu Met Leu His Arg
305                 310                 315                 320
Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Arg Ile Leu Ile Ile Thr
                325                 330                 335
Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu
            340                 345                 350
Lys Val Phe Gly Thr Glu Tyr Ser His Ile Leu Arg Val Pro Phe Arg
        355                 360                 365
Asn Glu Lys Gly Val Val Arg Lys Trp Ile Ser Arg Phe Glu Val Trp
    370                 375                 380
Pro Tyr Leu Glu Arg Tyr Thr Glu Asp Val Ala Ser Glu Leu Ala Gly
385                 390                 395                 400
Glu Leu Gln Gly Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly
                405                 410                 415
Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys
            420                 425                 430
Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Glu Ser Asp Ile
        435                 440                 445
Tyr Trp Lys Lys Phe Glu Glu Lys Tyr His Phe Ser Cys Gln Phe Thr
    450                 455                 460
Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr
465                 470                 475                 480
Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser
                485                 490                 495
His Met Asn Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile
            500                 505                 510
Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met
        515                 520                 525
Ser Ile Tyr Phe Ala Tyr Thr Glu Gln Glu Arg Arg Leu Lys Ser Phe
    530                 535                 540
His Pro Glu Ile Glu Glu Leu Leu Phe Ser Asp Val Glu Asn Lys Glu
545                 550                 555                 560
His Leu Cys Val Leu Lys Asp Lys Lys Lys Pro Ile Ile Phe Thr Met
                565                 570                 575
Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp Tyr
            580                 585                 590
Gly Lys Asn Ser Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val Gly
        595                 600                 605
Gly Asp Arg Arg Lys Asp Ser Lys Asp Leu Glu Glu Gln Ser Glu Met
    610                 615                 620
Lys Lys Met Tyr Asp Leu Ile Glu Lys Tyr Lys Leu Asn Gly Gln Phe
625                 630                 635                 640
Arg Trp Ile Ser Ser Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr
                645                 650                 655
Arg Tyr Ile Cys Asp Thr Lys Gly Val Phe Val Gln Pro Ala Ile Tyr
            660                 665                 670
Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro
        675                 680                 685
Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His Gly
    690                 695                 700
Lys Ser Gly Tyr His Ile Asp Pro Tyr His Gly Asp Gln Ala Ala Glu
705                 710                 715                 720
Leu Leu Val Asp Phe Phe Asn Lys Cys Lys Ile Asp Gln Ser His Trp
                725                 730                 735
```

```
Asp Glu Ile Ser Lys Gly Ala Met Gln Arg Ile Glu Glu Lys Tyr Thr
            740                 745                 750
Trp Lys Ile Tyr Ser Glu Arg Leu Leu Asn Leu Thr Ala Val Tyr Gly
        755                 760                 765
Phe Trp Lys His Val Thr Asn Leu Asp Arg Arg Glu Ser Arg Arg Tyr
    770                 775                 780
Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Pro Leu Ala Gln Ser Val
785                 790                 795                 800
Pro Pro Ala Val Glu
                805
```

<210> 78
<211> 264
<212> PRT
<213> Eucalyptus grandis

<400> 78

```
Met Gly Ser Thr Gly Ser Glu Thr Gln Met Thr Pro Thr Gln Val Ser
 1               5                  10                  15
Asp Glu Glu Ala Asn Leu Phe Ala Met Gln Leu Ala Ser Ala Ser Val
            20                  25                  30
Leu Pro Met Val Leu Lys Ala Ala Ile Glu Leu Asp Leu Leu Glu Ile
        35                  40                  45
Met Ala Lys Ala Gly Pro Gly Ala Phe Leu Ser Pro Gly Glu Val Ala
    50                  55                  60
Ala Gln Leu Pro Thr Gln Asn Pro Glu Ala Pro Val Met Leu Asp Arg
65                  70                  75                  80
Ile Phe Arg Leu Leu Ala Ser Tyr Ser Val Leu Thr Cys Thr Leu Arg
                85                  90                  95
Asp Leu Pro Asp Gly Lys Val Glu Arg Leu Tyr Gly Leu Ala Pro Val
            100                 105                 110
Cys Lys Phe Leu Val Lys Asn Glu Asp Gly Val Ser Ile Ala Ala Leu
        115                 120                 125
Asn Leu Met Asn Gln Asp Lys Ile Leu Met Glu Ser Trp Tyr Tyr Leu
    130                 135                 140
Lys Asp Ala Val Leu Glu Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly
145                 150                 155                 160
Met Thr Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Lys Ile
                165                 170                 175
Phe Asn Arg Gly Met Ser Asp His Ser Thr Ile Thr Met Lys Lys Ile
            180                 185                 190
Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu Glu Thr Val Val Asp Val
        195                 200                 205
Gly Gly Gly Thr Gly Ala Val Leu Ser Met Ile Val Ala Lys Tyr Pro
    210                 215                 220
Ser Met Lys Gly Ile Asn Phe Asp Arg Pro Asn Gly Leu Lys Thr Pro
225                 230                 235                 240
His Pro Phe Leu Val Ser Ser Thr Ser Glu Ala Thr Cys Ser Ser Ala
                245                 250                 255
Phe Gln Arg Glu Met Pro Phe Ser
            260
```

<210> 79
<211> 136
<212> PRT
<213> Eucalyptus grandis

<400> 79
Met Gly Lys Glu Lys Ile His Ile Ser Ile Val Val Ile Gly His Val
1 5 10 15
Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
20 25 30
Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
35 40 45
Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
50 55 60
Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
65 70 75 80
Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
85 90 95
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
100 105 110
Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
115 120 125
Lys Asp Gly Gln Thr Arg Glu His
130 135

<210> 80
<211> 229
<212> PRT
<213> Eucalyptus grandis

<400> 80
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65 70 75 80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
85 90 95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
100 105 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
115 120 125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
130 135 140
Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu
145 150 155 160
Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp
165 170 175
Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln
180 185 190
Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu
195 200 205
Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg
210 215 220
Leu Arg Gly Gly Phe
225

<210> 81
<211> 345
<212> DNA
<213> Eucalyptus grandis

<400> 81
taataaatga tgaatttatt ataaacgtat ccgtttgaga tttttgtggg tcataggtgt 60
atcaatttga aatctttgat agtaacaaaa ataattttag gtagtttatg tttttcatga 120
tataaacctt gaaagttaat gctactaaat tgttatatat atattaggca aattacaacc 180
ttaatgcaac agttaatgac gtgatactgt tcagattata gatacaatgg ttatccttga 240
atgaataaga agaagtccta agggcaagtg ctatgagctt gcacgactgc ttttgcgcca 300
tttttgttta ccagcccggg ccgtcgacca cgcgtgccct atagt 345

<210> 82
<211> 72
<212> DNA
<213> Eucalyptus grandis

<400> 82
cagtagggga cttgttcccc caagggcacg tgtcgttggt gaagctctgg cggtggatga 60
accgcgtggg cc 72

<210> 83
<211> 544
<212> DNA
<213> Eucalyptus grandis

<400> 83
actagtgatt tcgtcgtctt cgtcttcttc gtcttctgga acttcgttgc tccgagcttt 60
atcagaaccg gcgatggaaa tgaaaccctc gttctctctc cctcgctcct ctctttcttc 120
tatccaggag cgtttgtaca ctgggagtac agagcttctt gcgataccga aactaccctt 180
ggacgactgg ccttttttgcc tcgcgccccc tctctgagcc ggggcgcaat ttgtcccttt 240
cccagagcga agtgtcgatt ttgtccttcc acgaggcttt acctactccc atcgcccgag 300
ccccaagccc aggcccaaat gcctgttcct tgtggccctg ccaacattcc ctttgaaatt 360
aaaaaattaa aaaaaaactc tctgccaggc aaaagtaaag attaacacca ccaaaattta 420
taacaaattt atcattcatt aatttttcgtt aaatttttatt ttcaaattac tgagtcgaat 480
tacatgtata aattcacgga tgtatcggtt cgagatttta tcctctaatt atcattagtg 540
tatg 544

<210> 84
<211> 515
<212> DNA
<213> Eucalyptus grandis

<400> 84
gattactata gggcacgcgt ggtcgacggc ccgggctggt ctgccttcct ttaactcccc 60
ttttttgtaa ctttttaaaa tgtagtttta aatttaattt aattactttt tatattaatt 120
atttaccaca tcagagacaa aacaatgtct tttttgtatt ttctagtcac gtcaacatgc 180
aaaacaacgc cattttgcac tcaccttgcc ggaaaattgc cacgtcaaca atttggctag 240
agtggcgctt aagtgatcta ttttgctcca attttggcac ttaagtgtca ttttcctaaa 300
ttttagcact taaagtattc ctctatgtca agttttgaca cttggggtgt actttgtcca 360
atcataaacc gtataagttc actttaaaca aaaatggcgc aaaagcagtc gtgcaagctc 420
atagcacttg cccttaggac ttcttcttat tcattcaagg ataaccattg tatctataat 480
ctgaacagta tcacgtcatt aactgttgca ttaag 515

<210> 85
<211> 515

<212> DNA
<213> Eucalyptus grandis

<400> 85
actagtgatt tcgtcgtctt cgtcttcttc gtcttctgga acttcgttgc tccgagcttt 60
atcagaaccg gcgatggaaa tgaaaccctc gttctctctc cctcgctcct ctctttcttc 120
tatccaggag cgtttgtaca ctgggagtac agagcttctt gcgataccga aactaccctt 180
ggacgactgg ccttttgcc tcgtgccccc tctctgagcc ggggcgcaat ttgtcccttt 240
cccagagcga agtgtcgatt ttgtccttcc acgaggcttt acctactccc atcgcccgag 300
ccccaagccc aggcccaaat gcctgttcct tgtggccctg ccaacattcc ctttgaaatt 360
aaaaaattaa aaaaaaactc tctgccaggc aaaagtaaag attaacacca ccaaaattta 420
taacaaattt atcattcatt aattttcgtt aaattttatt ttcaaattac tgagtcgaat 480
tacatgtata aattcacgga tgtatcggtt cgaga 515

<210> 86
<211> 782
<212> DNA
<213> Eucalyptus grandis

<400> 86
gagggtttca tttccatcgc cggttctgat aaagctcgga gcaacgaagt tccagaagac 60
gaagaagacg aagacgacga cggcgacatg ccttgcttga acatctccac caacgtcagc 120
ctcgacggcc tcgacacctc cgccattctc tccgagacca cctccggcgt cgccaagctc 180
atcggcaagc ccgaggccta tgtgatgatt gtgttgaagg ggtcagtccc catggctttt 240
ggtgggactg agcaacctgc tgcctatggc gagttggtgt caatcggcgg tttgaacccc 300
gatgtgaaca agaagctgag tgctgcaatt gcttcaatcc tcgaaaccaa gctgtccatc 360
cccaagtcgc ggttcttcct gaaatttttat gataccaagg gttccttctt tggatggaat 420
ggatccacct tctgagctgt tggtcgcatt ctcctcagtg tttaccatgt atttcggccc 480
taaactctac ttctaggcct gttaaaagtg tctttttaa ggtaattctg ctattacccc 540
tcttaagtgc atcttatcag taaacatgga atatcctgaa ctttgattat atgccggctc 600
gtggctgtgg aagcacttct ttatgttacc accagcttct caggtgaata taagctttgc 660
ccagtctgtt ctctgggga tttgcttggt gggtagtggc aatcagatgg ttttgtcact 720
tttgtgcata tttaagtagt aaatgtccac gacagcccaa agagtagcaa tccgggtgca 780
ct 782

<210> 87
<211> 115
<212> PRT
<213> Eucalyptus grandis

<400> 87
Met Pro Cys Leu Asn Ile Ser Thr Asn Val Ser Leu Asp Gly Leu Asp
1 5 10 15
Thr Ser Ala Ile Leu Ser Glu Thr Thr Ser Gly Val Ala Lys Leu Ile
20 25 30
Gly Lys Pro Glu Ala Tyr Val Met Ile Val Leu Lys Gly Ser Val Pro
35 40 45
Met Ala Phe Gly Gly Thr Glu Gln Pro Ala Ala Tyr Gly Glu Leu Val
50 55 60
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Ala
65 70 75 80
Ile Ala Ser Ile Leu Glu Thr Lys Leu Ser Ile Pro Lys Ser Arg Phe
85 90 95
Phe Leu Lys Phe Tyr Asp Thr Lys Gly Ser Phe Phe Gly Trp Asn Gly
100 105 110
Ser Thr Phe
115

<210> 88
<211> 1521
<212> DNA
<213> Pinus radiata

<400> 88
ccttcaaaga caacagagaa agttatgcaa tatgctggca gctagctctt gggataatct 60
atttagcgat gggtttgtcg agaagttggg agcatttatt gtgaagcttc acagaaaaaa 120
tgtcgaatac atcaagcaca tgaagaagca atttgtgcca taggctatct ttagcctcat 180
ggatgttaaa ataatttctt tcttttccttc cttcttcttt cttacccacc aaaacacaaa 240
ataatagttt caaattttga attttcaccc aattttatga gaggacaaaa ttacttagag 300
tctttcactc tttaatttat attctacata agtacctaaa gaggctctcc gacaatcata 360
tgataccata aaagtaacct cgattagaga gcgcctctcc atacaatcat ttgattttcg 420
agttaaatca aaattatagg ctatttccaa atcaatctat cgtccaactg aaaatttcaa 480
atgaatggaa ccagcacgga gtttcgtagg aaatagaagt aataggtgaa aagaagcatt 540
gtcgaatttg aaagaatacc ctacgttttc atttcaaaaa ccatggtttt ttgtaagagg 600
gattaagttg actcaaggtt gtagaaggtt gacataacaa tagcatgcag gcacaggatg 660
catgtagtgc ccgtaatttg gaccaaccta gtaagattgt cacccgtttc aaatgactgc 720
ctacaagtgc atgcaaaggc catggaagtt gatggttagt gaaaagatcc ggagagacga 780
ttattccatc atgcaatgca catcgcacgc ttgctttatt actcacacga ccaacgttcc 840
cttcatccac ggaattaatt tctctaatcg atccaataaa ccgccttcga tgtcgatttc 900
caaatgaatt aaatcgttac atgcccaccc gacttcacac atgctccctg cacgtgcaac 960
caaatccatt acgcccaccg ggcccggccc tgctcacaca tcttgcatcg cccaactact 1020
ctgattttac atgaatatca atactattcc ctccacttat aaaatggcca aacgccctgc 1080
ttagttctca aagcagatca gagcctttca agagcttccg caaagatttt ctttgcgagt 1140
aatttgatcg agaaggatgt ctgcatcgaa cggaactaat ggtgttgtcg cagtcaagtc 1200
tcgccgacag cacagacctg ggaaaacgac agccatggcg ttcgggaggg cgtttccaga 1260
tcagctggtg atgcaggagt tcctcgtcga tggatatttc cgcaacacga attgccagga 1320
ccccgtcctc cgccagaagc tcgaaaggct ttgcaagacg acgacggtga agacgcgata 1380
cgtggtgatg tcggatgaaa tattggcgca gcatcctgag ctggcagtgg aaggttcggc 1440
caccgtccga cagcgactcg agatctcgaa cgtggccgtg accgacatgg cggtggacgc 1500
gtgccgtgac tgcctcaaag a 1521

<210> 89
<211> 2590
<212> DNA
<213> Eucalyptus grandis

<400> 89
ctgaaactgt cgctcggcga tgcataccaa aggctgaagg tatcagaatc taatgcagct 60
tatgtaaaag cgcgatcaat ttattgaccc cgacgacctt gactccatac ttcacgcctc 120
agctttgtgt tggatggtct tgacctctct caccctaaaa ggtagctcaa aagaatgaga 180
ctttccgtca tacttataaa ccgaccacca gcctctttca caaccgacat gggacaacct 240
caaatagaat ttttaacaac acccttgcac gctctttcta tccactttat tatgccatca 300
catgagcgtt ttccacgcgt aaatcggcta ccacccactt tcacacggcg gcgaaacgag 360
aaaaaggtcc taccttgac tccccccgcg tcccaaattc tcactcccga ccggtaaccg 420
agctcacaag tttcagcctt tcatcatcat cactcgaagg cagagagaag gacatacact 480
aaagacaacg aaacagtctc tccatcccgc catccgacac gatccacatt acggtacgga 540
acacatcccg cggagcaacc cgacgtccca aactcttcgc tgatcaaaac cagtccggtc 600
gactccgttt cgcgcggacg caacgtgaga gagggagaga gagagagaga gtaccggcga 660
ggggatgatg ctgtgcggaa gcgtcgtcgg gcgctctccc ggcgaacgcg tctctacatt 720
ccggcgacgg cgacggcgac gaaggcgggg aggggaatgc cgcggggttt ctgcaacgac 780
ggaagctcac ggcatttttc agagagagag agagagatgg cacgtcagag cgccattccc 840
ccacgcgacg ttccgccttc cggtattcct tccgggagaa aaagtgggca aattgcaata 900
gacaaaaaaa aaaagaaaaa aaagacggtc acccaaatta tttcttataa cacaaaaaat 960
cgtacctata taatatatct atcactaact tgtgcagtat gacaaattta cacatttacc 1020

tgaaactgtt tttataacat aaaaaattta aacatttttc tgtgacaata aatgttcaca 1080
caaatataaa actgggattt ttatttcaat tacaaattta gaataaatgc gcaacataaa 1140
tacaaattta tgatttttcg tgttggcaag aaagtttgag ataaatgtat cattgtaggt 1200
aaagtttaga gttttttttt atggctttta accaaaatgc acattttagt tccgagttct 1260
aaaagaaaaa ttactatttt cctttacatt tacttatgta ggtgtgtaat tataaatatt 1320
aattctcttt aggatttgta acaattcttt gagcttttgt tttgccttta ggccattaga 1380
attactaaaa agttaataat ataaacattt tttcgaccac ggtcaccatt catacctaac 1440
ttctaattat tgaaagattc tcgcatttga tcgaaatcca tttactctca taaatttgag 1500
gttttgaacg gtatctacca taagatcatg gtttattaca aaacacttat ggcgggtggc 1560
gcggacctgg cgagaatgtg gctacttaa tgatgaggat ttgagatatt ataccacgat 1620
ccataataat aaaggagcgc ggcaatcata tctttttttca tataaaggac gatttatttt 1680
ctatgctgtg agtatttgct cttggaatta taagatatta gagatcaaac ctatcaccaa 1740
cggtgatttg aaattaaaga agtccttgta tcacttacaa aaataaatat ataaaaaaag 1800
ctttcattgt gcacttgaat atttaaacat aaattattag tagtagataa ttttttaatt 1860
taactaataa tgagcactca tttttagaaa aatagttttc aaatcattca ttttctactt 1920
aaaaaaacca attgaccaac taaattagta tctctcattc agttggtgaa tgaatgactc 1980
gcactctaac ccttcacttg gcgagtcatt ctgtgtagac cagtctctgc aaatctagcc 2040
atgctcatct agcaactacc ttcaagcgca agtactttgt catgtagacc aaacgttgag 2100
caacacggaa tgaatcctaa cgcacttgga aaacaatcaa tccacgctac gcaagctaat 2160
gctcacacaa gcatcatgat acccgaagcc gaaaatacat gagtcgaaag acatcgaact 2220
ccgccgtcct cgcgaatcat ccgaatcgca tgtcacgccg ctcgacttgg tagcttaacg 2280
agccttccag tacctgctgt ttaaatgctt tgtcaatgtg attcgaatcc tttcaaagat 2340
cctgaaagtg cagcttcaaa aatggcgtcg accaaatggg cttgcgttgc tgcaatctcg 2400
ctcctactga gcctaggatc gagcgctgct cagaggtctc tccttatgag cagcgccaac 2460
tggcaagagg ccggtgagcc gacggatctg gacttacgtg gaggaattgc cggaaccctg 2520
gggtcatcaa gtgagggcgg caccatggcc agctccgaca tgggcggttt tggccaggac 2580
atgcctggtg 2590

<210> 90
<211> 1172
<212> DNA
<213> Eucalyptus grandis

<400> 90
actctcacta attctttagt tttccaattt agccccttct gtaattgctc atcttcttta 60
ccaaattctc taatttggcc ggcgaagggc tgacaaggga ttggtcatgt caccctcacc 120
aaaggttgcc gaaggtccgg tgacctcagc tgacggccac ctacaccaaa tctagctcac 180
tagcagccta agcccttcat caactctagt gaaaggtttt gagtattttt taataaaaaa 240
tatttaaaaa atatatagcg agagctcatt acaaaaaaat tttaaaaaaa aatctaaaca 300
ttacttgaac tcaaagtgac tttataaaga gtttttacca aaggatcttg gtttcatcat 360
ttgcactaca cccaaaaccc aatttctaag ttaaatcaaa cccactgtct aatagagata 420
aggtaaatgt tataaaccaa attccaaaat tccgaagcac taaatatatt tgctgatctt 480
ataatcgcca attgagaggg tctcattctc caagggattg tgacatatta gtaattgata 540
gggtctcatc cgtaggactc cgactcagcc gcgccacgtg actggatcgc tgaacggcgc 600
ggaaccagag gagcgtgatt acctaatatt ttctcctacc ttggccttga gattgaattt 660
cagaaaaaga aaaagaaaaa ggaacaactt cgccgactgt tctataaaat gcatgcgcca 720
ccccgacccc cacccacgca tcacatccat ccagcctcca cgacagacgc ataaacacaa 780
cacacgtcgg ttagagagag agagagagag agagagagag agagagagat gcttggacag 840
ttgtcgcacg agacggaaat gaaggtggga gcaggcaaag catgggagct gtatggcacg 900
ctcaagctgg tcctgctggc caagcaggaa ttctctaata ccatctgcga cgtcttggaa 960
ggtgatggcg gcgttggcac cgtcatcaag ctcaattttg gaagtttatc ctatacagag 1020
aagtacacaa aggtggacca cgagcgccgc gtgaaagaaa cggaggcgat cgaaggtggg 1080
ttcctggaca tggggtctcg ctgtatcgat tgcgattcga agtgataggc aaggacgagg 1140
aggagtcgtt ccgttattaa agccccccc cc 1172

<210> 91
<211> 446

<212> DNA
<213> Eucalyptus grandis

<400> 91
gggtgaaaac aattaatgag atcatttgaa ttaaggaaag tggaaaggcg gttttctgat 60
tggtacactg aaacaacagg aaggtggtgg aggccgcaat gatggaattt atccacttta 120
atcattttat gaaatcgata cactaacctt tgtttctcct aaacccaaag gcattaatcc 180
ctgtcctcct cactcgatct cgaaggccag aaggggggagg ccgagcctct tgctttttt 240
cgtgtataaa agggcctccc ccattcctca tttttcacca tcctccgttc gttcgttccc 300
ttccctttcc attgttgcgt ttaagccctc caatttttctt ttggcgtccc gtttttgggg 360
ctcccttgaa gatctcctct tcatttcggg atttcctgcc ttcgccgcgc catttgaagt 420
tctttttctg agagaagaat ttagac 446

<210> 92
<211> 2119
<212> DNA
<213> Pinus radiata

<400> 92
atcttattcc cacctcacat caataaattt tatacgattt taacatcttt aaaattaaaa 60
gaatcaagaa ggcatccagg tgataaagcc acgtccaata taaaatctcc tcggtggatc 120
ctttcaatcc agctacccaa tgcggcgaaa ataacgctga ttggactggg ctacactgta 180
atcacaaatt cccttccgtt tagatttcaa ctcgttgacc tacgagtatt ttatcgattt 240
aaaattatac aaaaaattgt ggaatgtttt acataagcaa aacttaaata atgtaaatag 300
cgatgatgct ttacttgtac ctaaaaattt cttccaaatt aaaccaaata tcaaatccta 360
gattgatgag ttccagtgga gtctgccatt ttatttcttt ctctctttca ttctttgcaa 420
cgaaaggaga aaatccttaa cacaattcga aaacgataat gattctggca aaagagaaaa 480
aaaacgtgaa gattagacac ttgttttgtt ttaaatgagc aatcacatgt gaatagagag 540
ggttttatgg gcctggtttt gtgtgcataa tttcttatga aagcgatgtg cctggagcgt 600
tgaagctcat agaacattgc aacaagagat cgagagtgtg ggttagaaaa ccgcaacaat 660
agtttgtgtc gtgtttttct atattcagag gtgttgtgtg gtaaatatct ctggatttat 720
ctcgaatgcg tcacttttac agacacagaa gctcagcgga aaccctcaac gctttaaggg 780
ccataaattt gctcagtttt aaaaattgtt tgatttccca ggtttgaata ttttcttttt 840
gttatcggaa gtggctctgc cttatgagta tcatgttctt ggttttgtgt tgggcgctta 900
ttgattcagg tatgtattat ttctagtcct ttttatcagc ataggtggaa tgttctgtat 960
tttatatttt ggggccatac acatggaacc gttgtcatta ccatgcttta tagataatgt 1020
ctctctgaat ttgtttttat aggcttttgc ctcctacgca gatttttaaa ggaaaataca 1080
aagatattta gccaattttt gttgttgtga ccttgaattt ctaaaaaatt taatggattc 1140
gttttctaaa ttcctgattc gtcaaaggct gaagggcgcg atagtaatag aaaatggacg 1200
agagtttatc ttttcatggc tggacacaca gaatttgtgg aggggattct ccattctggt 1260
ttatccaccg ttagttctct ctgtactcca cccttagttc tctttgtact cgagaccttt 1320
aatgattaac cctgcttatg ctgtcagtac tgaactcact tccagagccc caaaaatctc 1380
tcccaagttt gccttatttc ttaaaataat tcacaagtag aaaatgagat ttttgcaatt 1440
ttgtaactaa catttcccgg tctcctctgt atgttttcac cccttaatgt aattgaaatt 1500
tgcacccggg ttagattcaa agcggagaat aacatcgggg ccttgttcta gacagagatt 1560
tttcacaaat aacaggttcg aaggtatgtg tagacatctg ggtagttgta gaataaagac 1620
ggagcccatt aggtggatcc aatcgaagaa ctcagatggg aaaacagata aaaattatcg 1680
ggtggacctt cctccacatg ttaattatat atcaagtgtc gccaatcctt atgtgaaaca 1740
tttagtaaag cttcgccaga gcacttctta taggcattct gtgggctctg ttgttgtggt 1800
tggaagtact cctttaaggg aggtatctga atatttgcaa cagaagtcag taaaacaagt 1860
ggttgactgt ctgtttgtac aagatgttac tggcatacct gtgggcttga tagagacttc 1920
caggcgcatt gtgcatgtaa atcatttggt gatgcagaag ctagccggag tagagtctat 1980
agagcccact gaagcaattg gtgtaatcaa gcttcctagc agcttctaca acttggaatc 2040
tcttgaaatc actctagttc ccagatatgg tgctcgtcgc cacatcgtct gcttgtactt 2100
gatggcattc aggatcctg 2119

<210> 93

<211> 2571
<212> DNA
<213> Eucalyptus grandis

<400> 93
aaggtaactg gttcagcaga gcgcagatac caaatacttg ttcttctagt gtagccgtag 60
ttaggccacc acttcaagaa ctctgtagca ccgcctacat acctcgctct gctaatcctg 120
ttaccagtgg ctgctgccag tggcgataag tcgtgtctta ccgggttgga ctcaagacga 180
tagttaccgg ataaggcgca gcggtcgggc tgaacggggg gttcgtgcac acagcccagc 240
ttggagcgaa cgacctacac cgaacgtgaga tacctacagc gtgagctatg agaaagcgcc 300
acgcttcccg aagggagaaa ggcggacagg tatccggtaa gcggcagggt cggaacagga 360
gagcgcacga gggagcttcc agggggaaac gcctggtatc tttatagtcc tgtcgggttt 420
cgccacctct gacttgagcg tcgatttttg tgatgctcgt caggggggcg gagcctatgg 480
aaaaacgcca gcaacgcggc ctttttacgg ttcctggcct tttgctggcc ttttgctcac 540
atgttctttc ctgcgttatc ccctgattct gtggataacc gtattaccgc ctttgagtga 600
gctgataccg ctcgccgcag ccgaacgacc gagcgcagcg agtcagtgag cgaggaagcg 660
gaagagcgcc caatacgcaa accgcctctc cccgcgcgtt ggccgattca ttaatgcagc 720
tggcacgaca ggtttcccga ctggaaagcg ggcagtgagc gcaacgcaat taatgtgagt 780
tagctcactc attaggcacc ccaggcttta cactttatgc ttccggctcg tatgttgtgt 840
ggaattgtga gcggataaca atttcacaca ggaaacagct atgaccatga ttacgccaag 900
ctatttaggt gacactatag aatactcaag ctatgcatcc aacgcgttgg gagctctccc 960
atatggtcga cctgcaggcg gccgcgaatt cactagtgat tggcccgggc tggtctggag 1020
tggccaccat cggcataatg actaggaacc cggaacatca actgatggaa gaaaagccga 1080
cattcctcat caagagctcc tctcactcct tccccactac tactataggg cacgcgtggt 1140
cgacggcccg ggctggtctg ctgtcatatt tgtatatgag gtcctatgta tgcttgctat 1200
gtgacctcct tcatgtatgc tgtgaagaga gtgtagcagt aacatggcca tctgcgaaat 1260
atggattcac cttaaaatct gatgattttc agaaaacgag gaaggtgctt gccgagaaga 1320
ttgcacagct caattcagct atagatgatg tatcctctga gctccgaact gaagaatcat 1380
cagatgagat tgctgttgcc cctgatgaaa ttgaagctgc tgtttgatgg cccaaacctc 1440
ccaggcctac gatcatggtc atcttctgtt ttggtgcaat tggctctacc tttttggtgg 1500
cctccatata acagaataat ggttcatatt gtaaaatctt ctgtttattt ctaaagacca 1560
atgcactcag tttcttttga tatgattgtc tcgattgagg aagtgcatca ttcgtggtat 1620
gattatgcag aataccattt aactcagcag actttgtacc gtatcatcgc agcttttccc 1680
ttcttgtgta tgcataaatc tagtccttca ttgaaggtga tcgccgttac agtctggata 1740
gtgtgtgcca tcagatggca ctacgattag tgtggttgac atggtgtcaa cttgaaagcc 1800
aattggtgac gatggtactt aatgtaagat tggcagatgg tgagaacgag attttgctcc 1860
agaatggcaa agcaaggcta agttgtagcg aatcaaatga tctacgaacc atcctagctg 1920
gctgtgtgac cacacactga agttctattg aactaagcca gttatggatg atatgggagg 1980
agaaaattga gaaatccatc agatggagtg ttggccgtgt tgggcttttg tcgcaggccg 2040
atacttcgaa ttcaggcgta tttttattcc tgactgccgc ctctcccgga aagggaaggc 2100
ggatattatt ctctgaacga tttccaccat caactccaca tcgatctcca agccagaaat 2160
atacacaccc caattttctt ttaaatatat gggacatata tggtgtaggc tctcgcgcat 2220
gttaacacat aagctctctc aacaaaaatc tggctcgtgc ttttaaccga gaagttcacg 2280
agtcattgaa ggagtggcct ttaggggagg gagagagatg gattggtggt taaaatcagt 2340
ctgtggctca catttatacc gtggagatcc cccaacagca accttatccc attatatatc 2400
cccacaacac catattcacc actcgttcct tctaattggc ttccaaccat aattcacaga 2460
cacacatgta gtgaccaatg agaaaggaag aaaaatacag gctttcgaaa gctagtgcgg 2520
tataaataac ctgggaaaag caagccgctt gagctttagt ttcagtcagc c 2571

<210> 94
<211> 1406
<212> DNA
<213> Pinus radiata

<400> 94
aaagaggcgg aggaattgtc tagatggtca aaagtgaccg gaatctaagc aaaaaatttc 60
aaaaaatgtt gtaaaggtag cgtttgaatt gtgtttttga tggtggaaat ggattcaacg 120

ccatcaaaaa cgtctaagac acctaaaatt ttgaatttta acaactatat cttggattta 180
caaaaatcct tgccggattt tctctaaact ccttcacctt acgcaaaaga tatatatttt 240
tttgtgtgat gttgtgcatt ataagtttga tagtgaagta atgatatata tcctttatgt 300
gatggatgat tgaataatga atatattaaa tgaaataaat aatgatggga taatgaatat 360
attatatgaa ataaatataa agtaaaatgc tatttttaa tggtgttaat gatgaattag 420
tatcatcctt aaataatttg ttagtgaatt attaaaatga tgagttagca tggtcgttaa 480
ataaattgtt agtgaattat tatatttata tatttcctta ttagaaagtt ttttttttgt 540
aaaagttttc cttgaacttc acccatattt aattatcaat aatttatatt taataaatga 600
tatatataac ttctagcaga atgacacgcg acttgtatat cttttcattt tttaacccat 660
gaaaaccgat tagggtattg caaattaggg cattgccatt caaataattc tcagatgaaa 720
gattctctct aacaattaca aatgattatt tttttccatg agtgttgcat gttcgaacgg 780
tctgcccagt ctgtgagaga gcatagagaa ccctccctgc ccaatttgtt agagcataga 840
gaaccctact gcatgagtag taagaaaaat attcggtctc aattcggcaa agaccacctc 900
gaatggatga cttcaacgac aatctcatga tagtgttctg atcagcacca gttcacctat 960
atattttatc tagggtttag tttgcatgta tcaatcctct ggtgcactag gtaattcttt 1020
cctagtatca tatatcctta atactgtttt gtcttttaat ccatggctac catcagaaca 1080
agctcaaagc agaaatcggg agcatcagcc atcctcttgc ttatcgcgct tgcagggtta 1140
gtaaatgcgt gcaacgctgt gggtattgag ccaatgtgcg acactgtggt gtcgagtctt 1200
ctgaggcttc tgccatgcag gacggctgtt gatccctcaa ttgccgccat tccacttcca 1260
agctgctgca acgcggttga gtcagctggg cttcaatgcc tctgtctcgt cgttaacggc 1320
cctccttttc caggggtcga ccgcggcctc gcaatgcagc tgcctgccaa atgccatctc 1380
acccttcctc cctgtaacag ttagtt 1406

<210> 95
<211> 2546
<212> DNA
<213> Pinus radiata

<400> 95
ctggtagaac aagcagctca aggagcacca aggcacgagc ccactttgca tgttgtagac 60
taacgaattt tacattagaa taaaatatgt cgacaatatc gaggagatct tctccaaaat 120
ccaactcatt aatctctatt atgcacaaac gagtgatgtg tcgagactca tctgccaaca 180
agccatcaac atcaagaagg gaacggaata gagccaaagg gaacctaga gaccctcatc 240
cacataataa tgaaatattc cacgtgtgtt tttcaaaatt tgaaaatttc atgtattttt 300
tggttgattg gttgtggtct ggtttttcc aaattcaatc tagttcaagt ttttggagtc 360
gaccagttgg gtaaccagtc taattctggt aacattgcat tgtacttgat ctcaataaaa 420
gcatatagga tagaattatc ttctgtcttg atggtttcca tgagaaccaa ctgctatact 480
atgaaaaata tcaatgttcc acaatatttt tgggacaagg gaacacaaga ttgagtcaac 540
agttcaggac cccagaaaaa ttattcctga gttcgcagat tattttccta aaagtgaaca 600
attcaagacc ctagccaaat cattcccaag tccaagttat gtgacactgc gactaacaag 660
gcaagttgga agaaaccatc aatcaatctc ctagttaatg acagtccttg taagaagttc 720
aagaagatta acaccagaag aggtcatgct gactgctttt atccaattct ctctgctctt 780
caccaacaga aatagccaag atggttgtac ccattcccta atctaattta ttatatgaat 840
ttctctttat ttttctacat ataaaaaaca aaaacttttc ttgatggtca aacagaaaag 900
gcagttcgat tggatttaaa catccaaata cctcccacag attgagaagg ccaagcccca 960
atccaacagt ccatgatata atatttattc aatcacactc aagataatgc aatgaaggtg 1020
caccacgcta ttagattctg cacagaactc agatgactgt aattatcaac tttaaccagg 1080
agtaatttaa aaactcaatt gtgcttcagc tatgtggaaa aacttttggca ctggaaatgg 1140
tataaatgtt gttgaataag caaacatttt tcaagcactg aattcaaagt caagtcaaag 1200
gaacatctta cttgggctgt acaggaaatc tgaagtacaa aattagcgaa aaaacaggag 1260
aaagagagta gtcattacat gttataacat taccatatag gattttgtaa tacttcttga 1320
tatttcaact tcccgactga tgaaatgtat gccactacag aacaggtcag tcatgtatgt 1380
gagcaattag ccaaactagg tcctaaggtt caaccagtgc agacaacgct gtaactgaaa 1440
caaatttgtg ggacaattaa aaattctcta ccaggatagt tgtaccagta ggtgcccttt 1500
tcaaaccatg atttaaaaca caagggtggc ttaccacttg accaaatcat ttaataacca 1560
acccctcgaa catatcaaga aagaaaacat ctgcatataa gtaaattgaa agatgatatt 1620
taagaggcac tgccttaaat tttccatttg gacaaatcca cattgcttga taagcataaa 1680

accttggtta agagcaagtt tagggaacca tcaaatattt ctacatactt tacaatagtg 1740
tgtttataaa gctaatcaaa tgcttctatt taaatatata gcaacctaca caagaaattc 1800
actaggacag caatcacttg gccaatgtga ttaccaatat aaccatactt gaagagcata 1860
cataaatcac aaataatgat tcaattagaa atatcttaaa gataaactat tattcaatgt 1920
acatgttaca aagaacctca cctgtccgcc tttgaggagc aagtagacaa ctaaaagcgg 1980
aggttacatc ctgaactgaa cttgttctcc tctgttccaa gaacttgcat tgtattttga 2040
gtaacttcac tcgtgccgaa ttcggcacga gaaaacactt tgattgcttc cgcgggtggg 2100
ttttactttc tctggaatag ttagttccgc cgtttttgga agatttatca gaatggccaa 2160
aattcaggtg tcaaacggga gcgtcgtggt ggtggcggcg atgatattta tggtggcggt 2220
ggccatgcaa aaccatcacg tcgccgccca aagtgctgac tgcgcaccac cgcggagttg 2280
ctgagcccct gcgcctcggc ggtgggaaac aacccgcaga ccccactccc gaatgctgtg 2340
ctgttctcca gaccgccgat gtcgactgca tctgcgccct cgtcgaatca accataaaat 2400
tgccttccga atgtggtctt gacacccccc agtgcccaag cgactagatt ctcaagaccg 2460
tgactgagtg ttggtttcag agccagtaaa cattcattct gctaataaat gagtgtatgg 2520
agctttaata ttggaaaatg cttcat 2546

<210> 96
<211> 4726
<212> DNA
<213> Pinus radiata

<400> 96
gattactata gggcacgcgt ggtcgacggc cctggctggt cctaggacac cgtaatatat 60
aacctcgaca tggcttacaa agctttgact tgcattctca ttgggcttac aatggtgctg 120
ccaaaaatga aaaagtacat atgtacccct gttgaaatga gcagtaatag gcttgaacaa 180
tagtgaattg ctacaaaatt atgaatgcct ttctttgctt gaatgtgggc taaggagaag 240
tgggatttac atttgacttg caaatcctaa gacttgtcta gagctaagcc tccagaggag 300
gaaccatctt acatagtctt gagtctagag cggagaagat agccaaattt gaaaggaaac 360
ttttatttat ggggagaagg caaacaactt gaggggggaag gatgatcaat aagtagggta 420
agggaatcca caacagaggg cactaaggaa atgggggtgt tagaattggc aactagggcc 480
aaattccacc ttgggatagc tctctggatg gagatgatga ttgcattaga ttcctctttt 540
cgagaggacc aagattgata taaagatcat ctcatttgga caagcatagg tatgattttg 600
aatttatacc cactcatgca caatttttt aggtccgcca catcatcatg taggctcatg 660
aagcccaacg gacatgactc ttcgccctta tcgtcttgta taaatacaag tgtcctccca 720
cctcatttgg catcttcatc tcttacagat tctctcttct tccctcattg gttcttgcat 780
cattgggcat tctctctctc ccacgtgtgg cacaaggagg atgaaattac aagaccgaaa 840
ataatagaaa ttttgcaatt tgaccagcat tgaccatgac cttccaagca tcattcgact 900
tcaatttttt tgggttattt ttgtctcaac aagccgcata ttttggcaaa aaaatcgagg 960
cattctgggc acttcgacta caaaccaaaa ttgtaggttg actgcaaatt tcaaatagtt 1020
tgactattga cattgtcact gttttcgatt gactttgacc tcctaattag gccgagtttg 1080
actaggggag gctgatttgt tttaaggaca tttgattgat gctttgacta gcattgactt 1140
ttatagttaa ggttgaagtt tgactacagt tgactgcata aatttgcaga gatgttttga 1200
ctttgaattg ggcaagtcaa tttgaatttt gtactatctc tctattttga acatttgata 1260
taataataag aagattcgat caaagggttt tccccgcatt gggtttttc cctggcatcc 1320
gccaaatctg gtgttctctt gtctttgctt gtcttatgca ttttgtttca ttttctatct 1380
acttttactg tcaatgtgat tattgtcagt gttattggaa attggaaatt gtgattgggc 1440
tgctaaggaa cattgaagta aattgtgcta aacaaagaac ataccattgt taacgaaaat 1500
taacaaaggg gaaacacaga ggaatggttg caattgcaag attgtcattg attttgactt 1560
caagtgagga aggtcgcgtg gaggtcgcaa ggggagagga ataggagaga aggccctatc 1620
aacttgttca aggagagggg caatacaagg aatggaggaa ccctcaccaa tgaataatcc 1680
atgcacaaaa gtaatagaat gaacaaactt accacacgga agagcttcct tgttgccaaa 1740
agccttgcct ccgagacctg aatcctccaa tgcatcaaaa ttattgatca ttgaatcaac 1800
cacgattagg gccacttcct tggctaataa agcaattagt gtagcaaatt ctaaagctaa 1860
cttcaaagaa accttagctt tccaaaaaac aattgaaggg aggcaatgaa gatggcttat 1920
cacactaagc ctaaacatgc cccaccctat ggcatctaaa acatctaaaa gggattcact 1980
agtaatcgat cttttgtact tatgaaaaat tcccatgaac caattcgatc tcttccaaaa 2040
agccatctat gaggtcaacc tcaacctggc tctaatgttg attgagcttg taatcctagc 2100

cctactccaa tcttaagaac caaccaattt tatttccaat tgattcaagg acccctacac 2160
tccaaaagaa gcaagggaag gccaaggaga atggcccaaa cttgagcaga gaataaggat 2220
tctctgtgag ggtcgaaact aacatcccat tcacgtaaaa tcaaaccaga gagacctcaa 2280
ctccaactct tcttaatgat gaagcacaaa tattattttg agtgaaattt gaaaccaaga 2340
aaacctctca ctaatatatg gaagaggggc aatattcaac cattggtacc caaatcgcct 2400
caagacactt accaagggag ccaaccaaac aatcttacca caaaaccaac caacagtgtt 2460
tttacccaca agctcttgga tggaatccag gataatgtct tcaccaacaa ccatcttatg 2520
tctatccttg caagcacaaa tgcattgagc tttagatttg gagtgcataa atacaggggg 2580
gtatccaggg gggggagggg gtttgctaga accccagact caccaaggca tgaagacaaa 2640
atgaggagag agggatctag attgggggat gcaagttgat gaagcatgaa aaggcaatcc 2700
atcaccctgc atggcatatt tacgaaggtt gttcagagga atgagaacta atggatgaac 2760
aacagctggt agaacaagca gctcaaggag cgccaaggca cgagcccact ttgcatgttg 2820
tagactaacg aattttacat tagaataaaa tatgtcgaca atatcgagga gatcttctcc 2880
aaaatccaac tcattaatct ctattatgca caaacgagtg atgtgtcgag actcatctgc 2940
caacaagcca tcaacatcaa gaagggaacg gaatagagcc aaagggaacc ctagagaccc 3000
tcatccacat aataatgaaa tattccacgt gtgtttttca aaatttggaa atttcatgta 3060
ttttttggtt gattgttgtg gtctggtttt ttccaaattc aatctagttc aagtttttgg 3120
agtcgaccag ttgggtaacc agtctaattc tggtaacatt gcattgtact tgatctcaat 3180
aaaagcatat aggatagaat tatcttctgt cttgatggtt gccatgagaa ccaactgcta 3240
tactatgaaa aatatcaatg ttccacaata tttttgggac aagggaacac aagattgagt 3300
caacagttca ggaccccaga aaaattattc ctgagtttgc agattatttt cctaaaagtg 3360
aacaattcaa gaccctagcc aaatcattcc caagtccaag ttatgtgaca ctgcgactaa 3420
caaggcaagt tggaagaaac catcaatcaa tctcctagtt aatgacagtc cttgtaagaa 3480
gttcaagaag attaacacca gaagaggtca tgctgactgc ttttatccaa ttctctctgc 3540
tcttcaccaa cagaaatagc caagatggtt gtacccattc cctaatctaa tttattatat 3600
gaatttctct ttatttttct acatataaaa aacaaaaact tttcttgatg gtgaaacaga 3660
aaaggcagtt cgattggatt taaacatcca aatacctccc acagattgag aaggccaagc 3720
cccaatccaa cagtccatga tataatattt attcaatcac actcaagata atgcaatgaa 3780
ggtgcaccac gctattagat tctgcacaga actcagatga ctgtaattat caactttaac 3840
caggagtaat ttaaaaactc aattgtgctt cagctatgtg gaaaaacttt ggcactggaa 3900
atggtataaa tgttgttgaa taagcaaaca ttttagaaca tttttcaagc actgaattca 3960
aagtcaagtc aaaggaacat cttacttggg ctgtacagga aatctgaagt acaaaattag 4020
tgaaaaaaca ggagaaagag agtagtcatt acatgttata acattaccat ataggatttt 4080
gtaatacttc ttgatatttc aacttcccga ctgatgaaat gtataccact acagaacagg 4140
tcagtcatgt atgtgagcaa ttagccaaac taggtcctaa ggttcaacca gtgcagacaa 4200
cgctgtaact gaaacaaatt tgtgggacaa ttaaaaattc tctaccagga tagttgtgcc 4260
agtaggtgcc cttttcaaac catgatttaa aacacaaggg tggcttacca cttgaccaaa 4320
tcatttaata accaacccct cgaacatatc aagaaagaaa acatctgcat ataagtaaat 4380
tgaaagatga tatttaagag gcactgcctt aaattttcca tttggcaaat ccacattgct 4440
tgataagcat aaaaccttgg ttaagagcaa gtttagggaa ccatcaaata tttctacata 4500
ctttacaata gtgtgtttat aaagctaatc aaatgcttct atttaaatat atagcaacct 4560
acacaagaaa ttcactagga cagcaatcac ttggccaatg tgattaccaa tataaccata 4620
cttgaagagc atacataaat cacaaataat gattcaatta gaaatatctt aaagataaac 4680
tattattcaa tgtacatgtt acaaagaacc tcacctgtcc gccttt 4726

<210> 97
<211> 635
<212> DNA
<213> Pinus radiata

<400> 97
aaattctatg aaaaaaatcc aatcatatta aaagtccaat tgattagcaa ttttatgaga 60
aaaatccaat tatgttaaaa gtcactgagt gtggccgaaa ttgtgaccga aattgaatgc 120
aataaccgag ggtttttcaa accaaggtta agcctctcat cattggggtg tgtatgaaaa 180
tgtaatgggc atcgataacc ttttattaca acttcacgaa aattgcctct attcaatggg 240
tgtggatgaa aatgtaagtg cgcatcgata atggaaagcg atatgcagca aaatcaataa 300
acctgacttc ccatgtgagt gatgatttga tcgtacaact gatggtgtga agttactttc 360

agcttcacct tcgggcataa tcagggaagt agggccaagt ttgcttagta tcactctaat 420
ccccaacacc gtgattacta tcttcatcaa caatggccac cttcgtcatt actttaactg 480
gtgggataca gctactttac aactgtaaat ttgttgaggc agcctatcct cagcctatac 540
atactaatta ttgcagctcg attaggtatc tgctgtgaga atagctgtgt atctctgcgc 600
tggttgcagg atccaagttc ctctcagagc cctcc 635

<210> 98
<211> 468
<212> DNA
<213> Pinus radiata

<400> 98
ctggtaaatt gagattccaa attattgatg cgaagcttcc tcgtggctgg tcggtgctgc 60
tggcatccaa accctaaatg aaaaagaaaa aggtgtccgg acggattttt ttagtatttt 120
tttcttattt ttttttatgaa ccgtcggatt cgagatcgga cggcgatccg aaactgcaag 180
cgtcggccgt cggatgcagc atcggacggc aaagaaggaa ccctaaaacg cattgcaacg 240
tgcttggtgg gtggagggtc tatggccagt atatgttgat aacaagggag aggaagtagt 300
cctcttcatc tagtgcgagt ctctctgctt ttctacgccg ctgcgaagct gttctgtggt 360
gtttctgatt ctccagactc aggcagtcgt ttttgtaaga gaatttagtt catcatggga 420
aaggagaaaa cccatatcaa cattgtggtt attggccatg tcgactcc 468

<210> 99
<211> 222
<212> DNA
<213> Pinus radiata

<400> 99
atccaaaccc taaatgaaaa agaaaaaggt gtccggacgg atttttttag tatttttttt 60
tcttatttttt tttttatgaa ccgtcggatt cgagatcgga cggcgatccg aaactgcaag 120
cgtcggccgt cggatgcagc atcggacggc aaagaaggaa ccctaaaacg cattgcaacg 180
tgcttggtgg gtggagggtc tatggccaga tatgttgtaa tc 222

<210> 100
<211> 597
<212> DNA
<213> Pinus radiata

<400> 100
aaatgaggca gctaactatt tatttggttt tggcttcact gacttgttcc ttagtgtatt 60
aatgaacaat ctctttagac tcagagatgg tgagaaagat tctatgagaa atattcttgt 120
tattgcttcg actcatatcc cccaaagagt ggatccagct ctaatagctc caaatcgatt 180
agatagatcg atcaatattc gaatgcttgt tatcccacaa cgacaaaggg aatttcctat 240
tcttttatgt agcaaaggat tatactcggg aaaatgtccc gatgaatttg gatctataac 300
catagattat gatgcacgag ctctattagc tcaggcctct ctgctgctcc ttggattgca 360
atctcattct ctgatttgcc gtgctgtttg ctctgctcac ttcagcccag atggagacct 420
tcttgttcac atcggagtct gtaaatgagg gacacccaga caaactctgt gaccagattt 480
ctgatgcagt gttggatgca tgcctcaccc aggaccccga cagcaaggta gcatgcgaga 540
cttgcactaa aacgaacatg gtcatggttt ttggtgaaat caccaccaag gccgatg 597

<210> 101
<211> 669
<212> DNA
<213> Pinus radiata

<400> 101
cctggaaatg ctatattaac tcaacaaagg attttcagcc aatcacaatt tgacaggttt 60
gaaatgaaag attacaggca tttccaatgg aacagaatat aattacttta ttccctcaaa 120

gtatcgtata aaataaatct tttgctccac acactttgga aaatacattt tcaacaatgc 180
accgacaaac tttttctacc acgttatgga accatacaag ttaaatttaa acacgaatta 240
cgcgtatatt tctaataaat cgatggttga gattgaatgc cgtgggcgat tctcacgcgt 300
ccgattggga tcactagtcc atcactcatg gtctgcattg cctttaaatt ggcggggcga 360
ggaaagacca atgcgtcatt ggtgtagacg agctctatta gctcaggcct ctctgctgct 420
ccttggattg caatctcatt ctctgatttg ccgtgctgtt tgctctgctc acttcagccc 480
agatggagac cttcttgttc acatcggagt ctgtaaatga gggacaccca gacaaactct 540
gtgaccagat ttctgatgca gtgttggatg catgcctcac ccaggacccc gacagcaagg 600
tagcatgcga gacttgcact aaaacgaaca tggtcatggt ttttggtgaa atcaccacca 660
aggccgatg 669

<210> 102
<211> 230
<212> DNA
<213> Pinus radiata

<400> 102
atccacctcg gaatgaaatc actatgcaca ctccaccttt tttttggctt cttttctcgt 60
tgcctttacc atcagaatca agcacgaaga gtaaatatca cccatgcttt acaagtgggt 120
tggtagcatt agcgattccc ttcaccaaat gaacccttg ctggtgatga gtggacaacc 180
taaagttgtt tgctggtgat gagtggacaa ccagagtggg ggttggggaa 230

<210> 103
<211> 596
<212> DNA
<213> Eucalyptus grandis

<400> 103
actttgaaag ggtctcgagt caaagtgctc aaattgagag ggagaatttt agaacaaaat 60
cagatttgga gaatacatgc cattttaggg ggattttggg gatttcgcat atggcgtcgc 120
gtcgtcggcg ccttcttctt tacagattgt atcctcccat taaccgcgtg gacctgcact 180
gtaaccccga aacggtgggg gccaatttcg tctttccgcc tcctccactc agcttcgtgg 240
aagattaaaa tcctcaccgt ccgtgcaaac gccacgtggc gcgttagttt gcgcgtggaa 300
aggtcctcac gaaccgtaaa gggcaaaaaa aagggaaaat aaaaaaggag gaggaggagg 360
gaggaggaag aattgtccga ttgaaaataa gagtgcggtg gtgtggtgtg ggtagatctt 420
gaattgaacg agctcaatcc gcgtatttaa acccgccccg cttcctcatt cttccttgtc 480
catttcaact ctccctctct ccctctcttc tgcccctcga tcgatccagc gatcttccta 540
tttccggacg cggggagcag ctcctcttgt cgaaggttct aaattagtgt ggagag 596

<210> 104
<211> 653
<212> DNA
<213> Eucalyptus grandis

<400> 104
aaaatttcc tttatttct tttcattaaa aagataaata aataaaaaaa aaaaagaagg 60
aaaacacatc gaggtgaggc ttaaaggtgc taggcaagga ccaccaagcc tacacaaggg 120
tcggcgaccc tcaccaatgc tggggcgagg gtgagcaacc ctcatccaaa tctggagagg 180
gttgtcactc gagaaagggt cactggccct cccctaaccg ctactaacat cgttggcctt 240
cgtcaccacc gcactaacaa tgggccacta attttatatt tttcgtgata ttaatcctat 300
taaaaatgaa aatatctcct taattaatta agcttgtcag gaccgatgta aacaaaatta 360
atgtaaatgg acgcgccttt gacttgccaa caaactcgaa acgacgtttc ctccgtctga 420
taactatctc gcgacctccg acgacatccg acggtgcaga tcgggtcccg gtcaaccatc 480
cagatccacc cgattttctc ccggccctcg acaactccca ccaccacctc tttcctccct 540
ctttccttcc ttcctttctc accagatttt cccgagaaaa tcacagagag agaaagaaaa 600
acctcaccgc ctagagagag aaagagagaa agagggaaga gagagagaga gag 653

<210> 105
<211> 342
<212> DNA
<213> Eucalyptus grandis

<400> 105
agttgggtaa ccagtctaat tctggtaaca ttgcattgta cttgatctca ataaaagcat 60
ataggataga attatcttct gtcttgatgg tttccatgag aaccaactgc tatactatga 120
aaaatatcaa tgttccacaa tatttttggg acaagggaac acaagattga gtcaacagtt 180
caggacccca gaaaaattat tcctgagttc gcagattatt ttcctaaaag tgaacaattc 240
aagaccctag ccaaatcatt cccaagtcca agttatgtga cactgcgact aacaaggcaa 300
gttggaagaa accatcaatc aatctcctag ttaatgacag tc 342

<210> 106
<211> 342
<212> DNA
<213> Eucalyptus grandis

<400> 106
ggtctggaag ctcatctctc caatttggtg aagattacag ctataagagg tagctatgat 60
gtgctggcca aatgcaagtg atgaaatacg tggaccacca agtgcgaagg cattcgaaga 120
acgagggtcg aatttatagt gggcgaagga tgattaggtg gaatatgaca agaaaatagg 180
tttgaaagag aaataaatat tatgatagtg aagggtcttc acatggttag tttgatctgt 240
ccgagggtgt ccacccttgt ctgatccgca attgctcttg gtcgtgctga attttagagt 300
gtagccaaag taagaatttt cctttcactg tccggacatt tc 342

<210> 107
<211> 948
<212> DNA
<213> Eucalyptus grandis

<400> 107
ctgacaaatg caaatatcta aaaccattgg ttgtttggtg cttgcaagtc tggattaccc 60
cactttatgt ttcacctttc aataatgaat aacaaggtac tcgggaaaaa aaggaaaggg 120
aaattcgcac aaccaaagtt gctatgcaga agtcaactca atcctaatca agttgatgag 180
agtgttgggc cctattttct gcagcaaaca tgaatctcga ttcatctccc tcgcaaaaga 240
taaggaagct gcaaaagctt tcctcctaag tttgttggca agcaaattga ttttgtacca 300
gaaataaata caaagtgaaa cccaagcaat cacgcatggc ctgatttgtg ccatgtccat 360
ttgatctccc tctactattt ttcctgcttt ctcaagcaaa ctagttgctg taacagtgaa 420
tgatcccccg gctctctctc tctctctctc tctctctctc catttattcc atccatgttt 480
ttgcttttcg cacaacactt atcattgagg tgctaactac tgaattcccc taactaaaaa 540
ttggaacctc tcacctaatt tcattttctc ccactttgat gagcaccact ctctttccca 600
gatttcaaat aaattgccac tctctccctc ctctttcctc acacaaccaa aagccttctt 660
caagtaccac ttcttcactg tcctctcttc acaatccccc tcttaccaag agcaaagcaa 720
aaaacatgat gaagagactg tcatttctgc tcctactggt cctgctcttc caatgctcta 780
ccaccttggc tcagcctgcg gccgccccag ctccgcctgt gatagccccg gctgcacctg 840
ctacgcctgc cttaggcccg gctcctcctg tcttaggccc agctcctgca ggcccaaccg 900
acatcacgaa ggtcctcaag aaggtgagcc aatttacggt gctgctca 948

<210> 108
<211> 362
<212> DNA
<213> Eucalyptus grandis

<400> 108
ccatcactca taatcaacaa ggatatctca tcatgtcttc caaccaaatt aaaccccaga 60
catctctaaa gcagtatgga aaagaaaaca gtccggaagt ctctagctca aaaactgtaa 120

ccccgaccta attccggttg tctctgatta catcaattct tatgtcttaa cactccattc 180
gcacctccac aataaataga tcggcccttc atctcccctt accatcgaat ccaatcccaa 240
aaacacttgc tcagacacca tcaaatcctt cgcaaagtct ttttcttaca aaaaacaaac 300
gaaagcaacc atgaagcacc agttcattgt tctggctctc ttattcctca tcaacacagc 360
cc 362

<210> 109
<211> 326
<212> DNA
<213> Eucalyptus grandis

<400> 109
aaaaattaca atcaatggtt atcaatggat gttacaaagg gaggttacat atagaggtta 60
taaaagaggg ttacaaatag atgtctcaaa caattaccaa gcggttagat tgactccact 120
attttgacgg ttctcttgac tttactatct caacgattac tttatttcat catgttgacg 180
gttgcatcca tgattgttga cttcactttt tgtcgattcc ttcaagctgc tgattcttca 240
agttgccaat aattttattc ataaatgacg aaactctagc ctcatccatt aagtttgtta 300
cttgtccaca ataattaaat tcggta 326

<210> 110
<211> 296
<212> DNA
<213> Pinus radiata

<400> 110
tgctcccggt catgacaccg ccattctcgc tcttcatttc taattcaaat cacttggttg 60
ttgttcacac acacgggtct ttatatgacg agtgctgctg cgattataaa tagacggggc 120
aattacaaca aaaactcaca gcatttgaag gaagttggag tggtagagtg agaaatacac 180
agcctaatct gaaggaagtt cgagtaatag agtgagaaat ggatcttctt ctcctcatga 240
tgatgcttgt gatgatgggt gtagcaatgc ctactcattc tcaacaaatc actagt 296

<210> 111
<211> 723
<212> DNA
<213> Pinus radiata

<400> 111
cgttttacgc gggaacaatg aaaacagtac aatcgaaaga gtcaagtcgt gaggttcatt 60
tcgatgaagt tcccagagat tgtctcgttc aacgtttcct ctttttcgg gtcaagtcgg 120
gtacagaaga ccactttctt tacgcggtca agacaccgcc attctcgggt caagtcggga 180
ggtccctcct gctcttcctt tttccaaatc cgtaaaattt acagattttt ttaatgtatg 240
aagcccactt tctttatgcg gttgctccca gtcaagacac cgccattgtt gttcacacgc 300
acgggtcttt atatgacgag tgctgctgcg attataaata gacggggcaa ttacaacaaa 360
aactcacagc atttgaagga agttggagtg gtagagtgag aaatcatttg aagggagttg 420
gagtggtaga gtgagaaatc atttgaaggg agttgagaaa tatattggga atctctcttt 480
tttgcagcaa ttagatcttt cctttaatgc tttgagtggg agaattccga cagagtttgg 540
gaacctctct cttttgcggc aataagttgg agtggtagtt ggagtggtag agtgagaaat 600
acacagccta atctgaagga agttggagtg atagagtgag aaatggatcg tcttcttctc 660
ttcatgttga tgcttgtgat gatgggtgta gcaatgccta ctcattctca acaaatcact 720
agt 723

<210> 112
<211> 1301
<212> DNA
<213> Pinus radiata

<400> 112

actatagggc acgcgtggtc gacggccctg gctggtagcg acagagctgg ttcagtgacc 60
gttcgtgatt agccgcagta aaacaaaacc ctaaccgtaa ccctttcgcg cagattccat 120
ccttccccgt cctaccaaaa cccaaacttc ttgcccgaac tcaccttcta tgtattaatt 180
cttattatta tttaataata ataaatagtt aaacataaat ttataaatta attaattttt 240
atgattttta ttttagttta aaaatgtgac attgttatag attaatgctt atgaacgttt 300
attggccata attaccctaa ttaattataa ttaaaatata tagttataat taaaaaattg 360
tatattttat aaattgaatt aagaatttct gatgatattt catcattcaa ttccatctta 420
tcaaagttag agggaatagt taaccatgta ctagatctat tcatagctaa catttgccaa 480
gttcgtacta ggagacttgg attttttta aaacataatt ttggcagtaa aaagtgaatt 540
ctattgtttt gaaaacaaaa caaaatacag gaagcgtgat tgtggggttg ttgttgaact 600
tgcccgggca aaagaagaat gattagcggt agaggagtta gtagttacgt tcaactaaat 660
gcgtgactaa attatttatc ctccgccatg gaagcaggtg attcacacac aacttgctgc 720
acacattgct ctcaaacctt tcctataaat atccgtagca ggggctgcga tgatacacaa 780
cgcatttaat caaactactt tgattacttt ctgtgggttc tactttcttt gaatagtcag 840
ttctgctgtt tttagaagat ttataagaat ggccaaaatt caggtatcaa acgggaacgt 900
cgtggtggtg gctgcgatgt tatttatggt ggtggtggcc atgcaaaacc atcacgtcgc 960
cgcccaaagt gctgactgcg ccgccaccgc ggagtccctg agcccctgcg cctcggcggt 1020
gggaaacaac ccacaggatc ccactcccga atgctgtgct gttcttcaga ccgctaatgt 1080
cgactgcatc tgcgccctcg tccaatcaac catgcaattg ccttccgaat gcggtcttga 1140
gactcctcag tgcccaagcg actagggtct caagaccgtg actgagtgct ggtttcagag 1200
acagtagaca ttctgcctaa taaatgattg tatgagagct tttatatatg gaattgctca 1260
tatgctttcc tagatatgaa attattaaat tccatatgct t 1301

<210> 113
<211> 3070
<212> DNA
<213> Eucalyptus grandis

<400> 113
agcaccatca gcaaaaaata gatgggatag agtgggacac cacctgttca gtttgattcc 60
cttgagatga cctacagtga tagcttgatg aataagatgg gataatagat tcaccagagg 120
gataaaaagg tagggagata ggggatctcc ccgtctgatg cctcgggtag gttgaaaata 180
aggcaaaagt tcgccgttga atttgacagc aaaagacacc gtcgttatgc attgcatgat 240
ccattgtacc catgtagggt gaaatcctag agtgaggaga tagtccttta gaaagtccca 300
ttccacccta tcataggctt tctgcatatc cattttaaga acagcccgga attgacgtct 360
acattttctg actttaaatt gatgtagaac ctcttagact attaaaatat tgtcctgaat 420
ttgacgtcca ctgacaaaag cgctttgctc ctggaaaata agtacaggca ggtagggctt 480
aaggcgattg gcaatcacct tagaaatgat cttatatgcg taattacaaa gactgatggg 540
gcggtattgg tctaattgtt caggatgtgg taccttgggt attagggcta tgatggttcg 600
attgagattc ggtggtatga tgccagaatt aaaaaagtgc tgcactgatg agaatagttc 660
atcctggagt atatcccaat gatgctggta gaagagtcca ttcaagccat ctggaccggg 720
ggccttggta agtcccagtt ggaaagtagc ctctctaact tccttcttgg taacaggagc 780
tattagggac atattcatct cattagtaac aacctaagga cactggttca gaataggcaa 840
gtagtctcga tgtcccactg tctgaaatag atgtgaaaag taacctatcg tcatcatctt 900
caaaatttca ggatcgcgca cccaagcttg attgtcatcc tgcaacatac taatcttgtt 960
tcgttgttgt ctttgtatag ttgttgcatg aaaaaattta gtatttttgt ccccccagct 1020
gagccattta attcgagagc acatcgccca aaattattct tcttgctgcc ataactgtcg 1080
aattttctct tttaggtaag taaccaatga tgcgccatgt tgacaaaaag gctgattagt 1140
atgatcttgg agttgttggt gcaaatttgc aagctgacga tggcccctca gggaaattaa 1200
ggcgccaacc cagattgcaa agagcacaaa gagcacgacc caacctttcc ttaacaagat 1260
catcaccaga tcggccagta agggtaatat taatttaaca aatagctctt gtaccgggaa 1320
ctccgtattt ctctcacttc cataaacccc tgattaattt ggtgggaaag cgacagccaa 1380
cccacaaaag gtcagatgtc atcccacgag agagagagag agagagagag agagagagtt 1440
ttctctctat attctggttc accggttgga gtcaatggca tgcgtgacga atgtacatat 1500
tggtgtaggg tccaatattt tgcgggaggg ttggtgaacc gcaaagttcc tatatatcga 1560
acctccacca ccatacctca cttcaatccc caccatttat ccgttttatt tcctctgctt 1620
tcctttgctc gagtctcgcg gaagagagag aagagaggag aggagagaat gggttcgacc 1680

ggctccgaga cccagatgac cccgacccaa gtctcggacg acgaggcgaa cctcttcgcc 1740
atgcagctgg cgagcgcctc cgtgctcccc atggtcctaa aggccgccat cgagatcgac 1800
ctcctcgaga tcatggccaa ggacgggccg ggcgcgttcc tctccacggg ggaaatcgcg 1860
gcacagctcc cgacccagaa ccccgaggca cccgtcatgc tcgaccggat cttccggctg 1920
ctggccagct actccgtgct cacgtgcacc ctccgcgacc tccccgatgg caaggtcgag 1980
cggctctacg gcttagcgcc ggtgtgcaag ttcttggtca agaacgagga cggggtctcc 2040
atcgccgcac tcaacttgat gaaccaggac aaaatcctca tggaaagctg gtattacctg 2100
aaagatgcgg tccttgaagg cggaatccca ttcaacaagg cgtacgggat gaccgcgttc 2160
gagtatcatg gcaccgaccc gcgattcaac aagatcttta accggggaat gtctgatcac 2220
tccaccatta ctatgaagaa gatactggaa acatacaagg gcttcgaggg cctcgagacc 2280
gtggtcgatg tcggaggcgg cactggggcc gtgctcagca tgatcgttgc caaataccca 2340
tcaatgaaag ggatcaactt cgaccgcccc aacggattga agacgcccca ccccttcctg 2400
gtgtcaagca cgtcggaggc gacatgttcg tcagcgttcc aaagggagat gccattttca 2460
tgaagtggat atgccatgac tggagtgacg accattgcgc gaagttcctc aagaactgct 2520
acgatgcgct tcccaacaat ggaaaggtga tcgttgcaga gtgcgtactc cctgtgtacc 2580
cagacacgag cctagcgacc aagaatgtga tccacatcga ctgcatcatg ttggcccaca 2640
acccaggcgg gaaagagagg acacagaagg agttcgaggc attggccaaa ggggccggat 2700
ttcagggctt ccaagtcatg tgctgcgctt tcggcactca cgtcatggag ttcctgaaga 2760
ccgcttgatc tgctcctctg tggtgatgtt catggttctt ggatttgaaa ggtcgtgaag 2820
gagccctttt ctcacagttg gcttcggcat accaagttct tctcataaaa ggaaacaata 2880
agaagcgact gtatgatggc gcaagtggaa gttacaagat ttgttgtttt atgtctataa 2940
agttttgagt cttctgcata ctgatttcac agaatgtgta acgaaacggc gtatatggat 3000
gtgcctgaat gatggaaatt gtgatattct gtcttctttt tcagtaaatc acttcgaaca 3060
aaaaaaaaaa 3070

<210> 114
<211> 1227
<212> DNA
<213> Pinus radiata

<400> 114
aaatttcaag aggaagagat taattctttt aatttataaa attatataat aaaatattta 60
tatttaattt agatgataag tttatgaggt gtagaataga tagtgatggg tgtattattg 120
agttattccc ctaatgtgga gacaattgat tagaagttct atgagaaaaa tccaatcatg 180
ttaaagtgac ccctaatgtg aagacaattg attagaaatt ctatgaaaaa aatccaatca 240
tattaaaagt ccaattgatt agcaatttta tgagaaaaat ccaattatgt taaaagtcac 300
tgagtgtggc cgaaattgtg accgaaattg aatgcaataa ccgagggttt ttcaaaccaa 360
ggttaagcct ctcatcattg gggtgtgtat gaaaatgtaa tgggcatcga taacctttta 420
ttacaacttc acgaaaattg cctctattca atgggtgtgg atgaaaatgt aagtgcgcat 480
cgataatgga aagcgatatg cagcaaaatc aataaacctg acttcccatg tgagtgatga 540
tttgatcgta caactgatgg tgtgaagtta ctttcagctt caccttcggg cataatcagg 600
gaagtagggc caagtttgct tagtatcact ctaatcccca acaccgtgat tactatcttc 660
atcaacaatg gccaccttcg tcattacttt aactggtggg atacagctac tttacaactg 720
taaatttgtt gaggcagcct atcctcagcc tatacatact aattattgca gctcgattag 780
gtatctgctg tgagaatagc tgtgtatctc tgcgctggtt gcaggatcca agttcctctc 840
agagccctcc atggaagcgc agtcagtttc agttgttgag cagcgccccc atgccctact 900
attttcattt ccgttacagg gccacatcaa gcctttcatg aacttggcca agattttgtc 960
cagccggggc ttctatgtca cttttgccag taccgaattt gttgtaaagc gcctcgcaga 1020
atgtggtgaa agtatcgccc atcgtgattc gatggtgtgc agcgagaacg atgatgtatg 1080
taacataaaa tttgaaacag tgcccgacgg actgcctccc caccacgatc gcagtactca 1140
gaatcttgcg gagctcttcc aatccatgga agagaacgct catattcact tccacaagtt 1200
gatggagaag ctccagaatc ttcggga 1227

<210> 115
<211> 1169
<212> DNA
<213> Eucalyptus grandis

<400> 115
ttcattatat gattattacg tcataatgat cgatttctag aaatttggag acatatgtaa 60
attcaggagg aatttcaaga aacgcgcgtt actttgaaag ggtctcgagt caaagtgctc 120
aaattgagag ggagaatttt agaacaaaat cagatttgga gaatacatgc cattttaggg 180
ggattttggg gatttcgcat atggcgtcgc gtcgtcggcg ccttcttctt tacagattgt 240
atcctcccat taaccgcgtg gacctgcata gggcacgcgt ggtcgacggc ccgggctggt 300
ttcattatat gattattacg tcataatgat cgatttctag aaatttggag acatatgtaa 360
attcaggagg aatttcaaga aacgcgcgtt actttgaaag ggtctcgagt caaagtgctc 420
aaattgagag ggagaatttt agaacaaaat cagatttgga gaatacatgc cattttaggg 480
ggattttggg gatttcgcat atggcgtcgc gtcgtcggcg ccttcttctt tacagattgt 540
atcctcccat taaccgcgtg gacctgcact gtaaccccga aacggtgggg gccaatttcg 600
tctttccgcc tcctccactc agcttcgtgg aagattaaaa tcctcaccgt ccgtgcaaac 660
gccacgtggc gcgttagttt gcgcgtggaa aggtcctcac gaaccgtaaa gggcaaaaaa 720
aagggaaaat aaaaaaggag gaggaggagg gaggaggaag aattgtccga ttgaaaataa 780
gagtgcggtg gtgtggtgtg ggtagatctt gaattgaacg agctcaattc gcgtatttaa 840
acccgccccg cttcctcatt cttccttgtc catttcaact ctccctctct ccctctcttc 900
tgcccctcga tcgatccagc gatcttccta tttccggacg cggggagcag ctcctcttgt 960
cgaaggttct aaattagtgt ggagagatgg tgaagatctg ctgcattggt gctggctatg 1020
tcggcgggcc tactatggcc gtgattgctc tcaagtgccc gtcagtagaa gttgcggtcg 1080
ttgatatttc tgtctctcgc atacaagcct ggaacagcga acagctccct atctatgaac 1140
caggccttga tgcggtggtg aagcaatgc 1169

<210> 116
<211> 947
<212> DNA
<213> Eucalyptus grandis

<400> 116
ggtctggaag ctcatctctc caatttggtg aagattacag ctataagagg tagctatgat 60
gtgctggcca aatgcaagtg atgaaatacg tggaccacca agtgcgaagg cattcgaaga 120
acgagggtcg aatttatagt gggcgaagga tgattaggtg gaatatgaca agaaaatagg 180
tttgaaagag aaataaatat tatgatagtg aagggtcttc acatggttag tttgatctgt 240
ccgagggtgt ccacccttgt ctgatccgca attgctcttg gtcgtgctga attttagagt 300
gtagccaaag taagaatttt cctttcactg tccggacatt tcgattgcta catggaccat 360
cccgtgtcta cccattcttg agaaccttcg agtggaaagc atgaataacc caccttgtac 420
tatataggtt gccgaatatg cctagggcgc gaccatcatt gagacggagt tggggtgctc 480
cgctcggttc accaccacca ccaccaccac caccaccacc accaccattg ggcactgata 540
tagcgactcc accactaccc caaccgaggt tggcaaactc tagattgtac atgggatata 600
tcggagtagt tgaacatgat cagatcaatg gtagtggtta agactctaga aattattgaa 660
gcaatatgtt aaatcagata cgtgtgagaa agtgacttac taattgctat ggctttcatg 720
atacttaaac ttcaatgaat tggtaatgtg aagagcaatg tgatctccac aaatactact 780
agaaggccaa gtccttttct ttatgccgaa gtcctaaagt ttaatatttc aactctacct 840
atatcaaatt tgtatgcaaa ttgcataatc gcactgattt ctatggtttt attaatctag 900
ataagaactc tctccaagac attaactaat taagattgac cccattt 947

<210> 117
<211> 1766
<212> DNA
<213> Eucalyptus grandis

<400> 117
atccagatcc ctacgaactg gattcacaca gtcactgctg taagctctgg ttttttttag 60
cttaggaagc aggttatgat caaacatgat taaaccatcg cgtgttcgcc agccatcaga 120
aatggaaagg caaatgttgt tatagtgatg gacagatcat gctgagatga ttgattatga 180
atcttactga tgactgtcat ttatgttatc gcactctgtg tgtgtgggtg tgtgtaatga 240
gtaatatcaa attaaccaga cgataggtgt tgaagattag ctgttgggcc accgtggcga 300

```
aaggtgtctt atacaagcca tcggcagtga cgcagaactg tagagaaccg ctgtaacaag     360
tcttcgaatg cattctttta atgtacagca cgacatgaag ggggttcgag tgtagcgaac     420
agttcgtgcg agaaagatca ttttcaatag cataaaagag tctgctttct gctgcaaaca     480
tggaaagaac ttacatttca atcattgagg agaagattat aacaaatcct aaatggttga     540
gattttagtt agtccattcg aactaaagtg gcgaagatgt cagtttttca agtggatgat     600
atttctcatg tatgttccgc agaggcaatc accttgtttg taactagaca tctagagaac     660
ctaacaagga ttgatggggg tgaggtgaaa tgtctgtttc ctctttaata tggatccagc     720
gatgccttac agagcggatg gatggcactg gcaagtctta atccttagct cgaatgtttg     780
attggtaaca gatgcctttt ctttcttttc aatcacagct gacaaatgca aatatctaaa     840
accattggtt gtttggtgct tgcaagtctg gattacccca ctttatgttt caccttttcaa     900
taatgaataa caaggtactc gggaaaaaaa ggaaagggaa attcgcacaa ccaaagttgc     960
tatgcagaag tcaactcaat cctaatcaag ctgatgagag tgttgggccc tattttctgc    1020
agcaaacatg aatctcgatt catctccctc gcaaaagata aggaagctgc aaaagctttc    1080
ctcctaagtt tgttggcaag caaattgatt ttgtaccaga aataaataca aagtgaaacc    1140
caagcaatca cgcatggcct gatttgtgcc atgtccattt gatctccctc tactattttt    1200
cctgctttct caagcaaact agttgctgta acagtgaatg atcccccggc tctccccctc    1260
tctctctctc tctctctcca tttattccat ccatgttttt gcttttcgca caacacttat    1320
cattgaggtg ctaactactg aattccccta actaaaaatt ggaacctctc gcctaatttc    1380
attttctccc actttgatga gcaccactct ctttcccaga tttcaaataa attgccactc    1440
tctccctcct ctttcctcac acaaccaaaa gccttcttca agtaccactt cttcactgtc    1500
ctctcttcac aatccccctc ttaccaagag caaagcaaaa aacatgatga agagactgtc    1560
atttctgctc ctactggtcc tgctcttcca atgctctacc accttggctc agcctgcggc    1620
cgccccagct ccgcctgtga tagccccggc tgcacctgct acgcctgcct taggcccggc    1680
tcctcctgtc ttaggcccag ctcctgcagg cccaaccgac atcacgaagg tcctcaagaa    1740
ggtgagccaa tttacggtgc tgctca                                         1766

<210> 118
<211> 1928
<212> DNA
<213> Eucalyptus grandis

<400> 118
ctggttccac gtcaagcacc tcctggagtg acaaggaaat gccaccggaa aatcaagatt      60
gctgttttag gctcactttt ttcctgagct aagtgggtcg catttcaaga aacagtagaa     120
gttacgttct ccatggaaac tcgaaaggat aaaaattaag aaacggaagc tccatgagaa     180
cgatgggggt cagcatcact cctattgtat tgtgctctca ttatctctgg cctacttgag     240
aagtgatctg ggattcgcta ttagtgaaaa caatcgcagg ctaactaaga tcttttatgc     300
taatcatatg gagaaatatc cctcttaagg gaagcatatg agtttttct taggatgact      360
acgcttattc aaaacctatc atacacgtca tgccaataat acccacttgt tgttccttta     420
ctcaggatcc tcgatagcca atactaattg gcaagaacct tgagtaacaa gctgaggtat     480
acataggcct atcattcatt tactagactc gattgcaagc acacatgatg cacatttata     540
tcagcaatca gcaatcatat ttccgaaaat tgtctctcag agaaaaagag agagagagag     600
agtccatagt atgtcatagc caaaagaaaa attagcaaca agatctcgag gtattgttga     660
aaggtagggc aatatcaaga attccattgt aattaatgtg tctagacaac atctaagaaa     720
aaaaagtgaa agaaaagagc tatatagtta ataatattta tacatgttgg agataaactt     780
gagttagagg tttatgacct cctagattga ttaaacagac caaatagtag taatcagggc     840
acttcttaaa tctactaata tattgttcaa acatgacttt taacctatct tgattagaaa     900
tgagtgttca aagaaaacta atcatgcata tattttgtcg cccaatcacc ctagggtgga     960
aaaaaggcta tctactcaac aaatgctaaa attttacggc tacacgtggc cacagttgca    1020
gtacaattca tctcaaggaa ggactaaaac tgcaaagaga agaagactac ataggaaaaa    1080
ggaaaacaaa gaagccttga agtaaagagg agcataactc actcaactga gtgtgttcgc    1140
caatgtggca aagaaaaagc ctctaagatc ctcacaaatg gccacgtgga ctcacacggc    1200
accctataca agtactacta ctactacagg actatgccag aaggagaagt gttagcgtga    1260
gtaccacgtg cgcacgcaga atctaagcct agcaaaaact atgctgagtc aagcagctcc    1320
cccacccatg aagatagtac tgtaatgtga ctcttgacag cgaaaccaaa cagtactcca    1380
agagaaaagc caaagcagca aaaatggggc ccgcagcaag aacctctgac tcgacctgga    1440
cccaccaaga acaacagcca gccacaaaat aacgtaaaga ctttttgcgg ccactaactc    1500
```

ctcgacaagt ggcactgctt ggattccctt catcttgcct tcacttaacc cccaccctcc 1560
ctcacactgc attcacttca aacactcccc agtttcagag tttcattgag aaatatgttg 1620
aaggaagaca cgagtggcag cggcggcagc agcggcagcg gcagcggtgg taatagctgg 1680
gcacgtgtgt gtgacacttg ccgctcggca gcatgcaccg tgtactgccg tgccgacttg 1740
gcttacctat gctccagctg tgacgctcgt attcacgcag ccaccgtgtg gcctcgcgcc 1800
atgagcgcgt gtgggtgtgc gaagcgtgcg agcgcgcccc ggctgccttc ctctgcaagg 1860
ctgatgcagc atcactgtgc accgcctgcg atgcagacat acactcagcc aacccgcttg 1920
cgcgccgc 1928

<210> 119
<211> 602
<212> DNA
<213> Eucalyptus grandis

<400> 119
attgggagga agtagagtgt gctgtgtgag attggtcgat gagctggctc ttgtggagat 60
ggcaagtgat tgtggcttct gtgatgcata tatataggca agggacgtga tgcggaggaa 120
gtatgtatca tcagcttata ataatgattg gtcagtttgt aagtgaatat taagggcctc 180
atgggtgttg gttcacggcc caaggcgggg cccactcacc gggggattta tcgtgtaagg 240
atacatccag ggtcagggtg tttggggaca cactttgcca tcttatgtgg gcatgatcag 300
attgagaaga atccgatcct tctttttcct aaaccattga acccaccatg agaatctttg 360
tttggaggga aaaataaaaa aatagattga gacgtattct aggagaggat agcaaaagaa 420
tgtgactttg tttgtttgtg tatcggattg atctaaggaa aaaagacact aaccgttcta 480
caattttcat acaactcttt catttaagca ccgtgacttc caaaaatcga tcatccttat 540
acggttggaa atcacacgtg gcattgctgt aaaagaaata gttgatgggt ctcattgaag 600
at 602

<210> 120
<211> 1326
<212> DNA
<213> Pinus radiata

<400> 120
aaaaaaggga aacattatac caaattttat gatatctttc aacaacatac tcttctatat 60
atggtgcctc ctctgatgga cccttgtcaa ctttctcttt ttatgtgtaa tgcctcaaga 120
gcccccactc acaagataat atcttttcca taatataata tatattccta ttgaagcagt 180
cttttgatgt accgagtaca ctactcatgg tgaaggccgt gtcttgcagc ttttcccatg 240
gtttattttg aaagtaatag tactggacct catttgcaac gacacataat attcttactg 300
acgacacttt gtttgatttc ttatagaaaa atgcaaggtg gcacaaaaag atggaaagcc 360
cgacctatca agcatacgaa gggtcatgtt cacaccctct gaaatcttca gagtctcacc 420
ctatgttgga cgctaatcaa tgggatcacg ctgaaacata tcgtaaatga cgaatcaatc 480
aatcaatcat tgaaaaatat accagataac tcctacgatg gaggggatta tttgcgtacc 540
ctccgcgtgg gtgggcacat tgggcaggtc ctttggtaag tcttggagac agagtcacgt 600
ttccataatt gaagtggaca tttatgaatc tttcgaaagt tgtagaactc ttaattttcg 660
acggaatagt ttgacacgtt ttgtacgatc tggtttttcc ggggaacgcc aattttggtt 720
tctgaaggac agcatttaca atattgtctg tcgttgacca ggacagctgg ctcggaactc 780
gggtttccga tgcgcaggaa gcgcattgaa atgagaatat aatctagttc tacctgtgga 840
gctatcacaa aatactaaaa ctggtggaca tacctcttgt ctgttctcga aatcggccaa 900
aatgggaaag aagagggtag agctgaaacg cattcaaaac cctagcagtc gacatgctac 960
tttctctaaa cgcaagaatg gattgctaaa aaaggcgttc gagctttctg tcctctgtga 1020
tgctgaagtc gctctcatca ttttctctga aactggcaag atttacgaat ttgcgagcaa 1080
taacgatatg gcagcaattc tgggaaaata ccgagtacac gaagaaggca ctgaaacgtc 1140
cagtccaaca tcgcttcaaa acgtaaagta tcatgaatca gggcttgaga aattgcaaga 1200
gaagttgacc gctttgcaaa agaaggaaaa gaacttgatt ggtgaagact tggaggtatt 1260
aacaatgaaa gaactgcaac ggcttgaaaa acagttacaa attggcataa aaaggttagt 1320
gataga 1326

<210> 121
<211> 1504
<212> DNA
<213> Eucalyptus grandis

<400> 121
atccactagt tatataaaaa taataataat atcaaatata tctcgtgatt tatgtatcta 60
tgaattatat atcataattt ggtaattaga catgtgggcc acttcaatgc atggacattt 120
agttcatctt gactcaatac tcaacctcaa cttaaataca tcctgattat tgatggcaac 180
cgaccaattt gacgtagagg ggacaaggat tgcaacttgg gtttgtgtgt tgggcaaagt 240
gagctcaaat aactcatgag ttcctcaact tgtttgtgtt gcccttgctc aacaatcata 300
acaaagctag ctaaacacaa atgaacaatc aagtatatcc acaaaaaaac aaaaacaaaa 360
aaacaagaaa acccaagcac tgataagaaa atctaaattt ccaccaaaaa tgacaaatag 420
acattgccta tactttcatt tgccgattat cgaaggaatt tacgcataga atgacccatt 480
tttttgacaa atgagatttg catcattatt caacggcatt tcgtggtata ttccatctgc 540
atgggtgttc caaaaatagg catcgaatat tcttctggtg gaaaaaaagg ggcggggcgt 600
gaaaaatgaa agaaagaagc atcaagtggg actgaatcgc cgagtaaatc gtgccgagcc 660
gtacgtcaga agatacacac ttggctcaag tgggcgtcaa agcgatggcg cttgattggg 720
acctttgacc tttcgtcacc tccccatcct ccgtcctcct ccctgtcgcc cgttcattcc 780
ctccctccaa taaaaacaaa aaaacaaaaa aacaaaaaaa ctgtgctctc ttttactcgg 840
tcaaaacctt aaaagaagcc ccccgcccac gcaaatccac ttgccacgtc accaaatcca 900
aatcccacac gtggcgcaca ctgaatcgca ttcaacttgg aacagctggc ggggttttac 960
ttggagtccc agtcacttag attctttgca gccatgacga tgacagtgac gctggctttt 1020
ctgcgtcctc tccgtaggaa ggaactccca gtacagactg gatcctccta atcccgtgtc 1080
ctcttcctga caatccccgt tcatataaag gaacccgaac tcactccctc cgctcccaat 1140
tcaagcacat gttctactcc accttcatct cacaataaaa accagcagtc cagcacgagc 1200
acattatcca cttccactcc agaactcaag cgcagacgta ctccaatgaa ccacttcttc 1260
tcttcttact ccgatcccag ctcctgcagc ctcgactttg ctgaagcgtc gtcctcctcg 1320
tcgccgctgt ccgatggcag gagtgctatg gtgcccggga acttttctga tgaggaggtg 1380
ctcctggcgt cgcaccagcc gaagaagcgc gccgggcgga agaagttcca ggagacgcgc 1440
caccccgtgt accgcggggt gcggcggcga agctcgggca agtgggtctg cgaggtccgc 1500
gagc 1504

<210> 122
<211> 1202
<212> DNA
<213> Pinus radiata

<400> 122
caataattat ctcaattaat atagtctaac acaatttgaa tttcaaaata aacttaccta 60
tcaaatttga aaattttcac acttgtccat tcgccatcct atctttacag ctgccaagaa 120
aaaaattgac aaatttgcaa actaatatct tttatctata ttggatgagg gcaaatcatc 180
caataaaaag aaaacacaac aaaataaagg aatatccttt gaaaatactg ccagctgaat 240
ttccaattca actaaaactt tgaaccgtcc ggaatgagaa actcaattct cctctccgcg 300
tctttaggag taaactatgc tgtacaatcc gttaatttct gacacacaat tcctcacgat 360
aaaagaaaaa tctgtcagtc tatcgggtag ctggcggcac accgtttaac ggacgaccgg 420
tagctttgcc ctttagatcc accatccagt aactggcaat aggcggtggc ttactggccc 480
accttgagct tgccaattca ccgacatgaa cgcgtgtcag acggaagaag caacacaatt 540
ggacacagaa atacgactcg tttgcaacca caaaggaacc atccgttgtc gtgtattaat 600
taaaaaatga gatgttaaaa attcaaaaaa tgatttataa tagaaaaatt atatatatat 660
ggatctgaat atgcttctcg ttgcttgttt cgtaggataa ttcagaggga gaagtcgctt 720
atattctata ctgacaccca ttccttgaag gaagcgctcc agtgttagag gccctggggt 780
ttgaaagctg attggtagca gggtcttcta tcagtgtacc tcctggttta attttaattt 840
ctatgaatga catgcatcct tattaggaca aggggtttga tatatcaatt gcaaagggtt 900
tgagagaagc cagggtttgg tctttgtgtc aggcgagaat ttgttaatct ccagacgcca 960
tggacgctga attatgggcg gctcgtgtca cggcagcaaa gcgccatcac gcagttcatc 1020
attatcatca tcatacagat cggcagttta actttgatga attggagggc gatgatgaca 1080

tacgggcgga tttcacttgc ccattttgtt ttgaggattt tgatatcgca ttgctctgct 1140
gccatcttga ggatgaacat tgcatcgaca caaaaaatgc gctatgtcct gtgtgcgcag 1200
ct 1202

<210> 123
<211> 1397
<212> DNA
<213> Eucalyptus grandis

<400> 123
ccttcctaaa gagctaccat ttctcctcat catccccgcc gccagaagaa gaagaagata 60
tttgcgatca tgaccatcag gatgatcatg atcgggtcag tggatttaag tggaagctca 120
agaggtcgat gaagggtttt aatgagtcgg cagcgggaat cgtaatggag gtccgtcgag 180
gactaacgtc ccagaggagg ctcaaaatca gggttttcag ggccaagctc aatcttcact 240
cttctttggt tgccttaacc acgagatgtt tcattccttg gtttagcaaa gttgagcatg 300
cgcagtgacc cacagttcaa ttagctttca ctccagaagt tctctatgtg aatatagttt 360
gaggttaaaa aaggttgcaa ccactctcct tctaagcacc atatgctcct gtcaatatcg 420
attgacctct tgtgagtttg gcaggaagta ctcatgtcca cagaatttct tgaaaataat 480
taacactttt gtcgtaaaga acgtagggta aaaggagaaa ttctacttct cgacatccta 540
cttttacctc ttcaaaatta tgcgattaat accatacgat acgtcttgac gatcctatct 600
cgcatggcac gtgttattgt caaaggtatg attttgattt ttcgacaatc aaagcaacgt 660
caatccccat tcaagattga tgtactatgt cgaggaacca taaaggatct gttctctctg 720
aggacggctc acccacatgg ggggtctgac cccaccaaag acttggtgga tgttgtggat 780
ttcatgcttt tgattcgggc caaaactcat atctccttat cttctctcgc cccttgactg 840
tccaccaaac actctcgggt atcttgccct caccaatcat ccacgcgcac aaacagacga 900
acgcaacaat atctctctga ccctcctctt tctttcattc tccctccacc tcttgatact 960
ctatttctct tgttctctta attgcgaaaa ttactcttga acttgtctgt ttgtcctctc 1020
agcgtggcct gagatgggca tttttcaaaa ttaaacattg ctgcttggtt tagagacttc 1080
acttgatgag gttgataggt gaagaagaag aagaagaaga agaagaagaa gaagaagaag 1140
atgaagatac agtgtgatgt gtgcgagaga gcgccggcga cagtgatatg ttgcgcggat 1200
gaagctgcgc tgtgtgagaa atgtgatgtg gagattcacg cagcgaacaa actcgcgagc 1260
aagcaccaga ggcttctcct caactgcctc tccaacaaac tccctctctg tgacatttgc 1320
cgggagaagg ccgcgttcat cttctgtgtc gaagaccgag ctctcttctg tcaggactgt 1380
gatgaaccaa tccattc 1397

<210> 124
<211> 1142
<212> DNA
<213> Pinus radiata

<400> 124
atctgataca attgtgaagg tgttattaat aatattttca tttctctgaa atctaggttt 60
agtcaattac atatttgata attttcttca tttccttacg caaatgattc catgaacgaa 120
attttgtttt ttgatttttt tgtttcgttt atttctacca cgtgttgcat ttatatttga 180
aagcataagg agcacagtta gttttgatac ctgcaatgcc acgtttttc tgcaattcca 240
tcttccacca cacattcaaa gataatgtcg gtcatcacat tcttcagaac gcaatttgtc 300
atcaatgggt cacatgctgc catcagtatt ctgaatttc aaagcagaca aacccaaata 360
cacctggatt gcagtgggta cattatagtg acatgataaa tatcccacat cacattcttc 420
agaacgcaat ttgtcatcaa tgggtcacat actgccatca gtattccgaa ttttcaaagt 480
agacaaaccc aaaatacaac tggagtgcag tgggtacatt atagtgacat gataaatatc 540
ccacatcaca ttcttccgaa tgcaatttgt catcaatagg tcacatactg ccatcagtat 600
tcttaatttt cacagtagac aaacccaaaa tacaactgga ttgcagtggg tacattatag 660
tgacatgata aatatcctac cgttttgata gtaaacttga gctgcaagta aactacatgt 720
gcactcatgg tggggcttgt gctgccaatt gccctttaaa atggagtcca tcaacatctt 780
tttaacataa gaattcttta gactgggagt tgatttgagc tttattttgg tgtatcatct 840
tgtagtctga aaaagaagat tcacagtacc agcttaatta tttcatcatg gccactgcaa 900
ccttcataga tatcttgttg gccatacttc tgccaccttt gggagtcttt ctcaaatatg 960

agtgccattc tgaattctgg atatgtgtgc tgctgactct tttggggtgg ctaccaggga 1020
ttatatatgc cgtctatatt ctcaccaagt gaaaatgaat attctttgtt tggagcttgg 1080
tgccacttaa ttgtcatgag taaacataat tgaatttgtt tattcacttg ttttttatgc 1140
at 1142

<210> 125
<211> 1489
<212> DNA
<213> Eucalyptus grandis

<400> 125
atcattgcac agatgctggc ctatcaagcg tccatcgatt aatgtcatga tgattcgtgt 60
catcaatttt cccatagcga gtcagcgacc accgcatgca cgatgccgat gtcgccgtgc 120
gaaaaacatc gagcagacgg catgctaaag acatgcattt cggtcctctc tgatggtgaa 180
ttgcaatgca gaagagactc ggatggattt gatttcaaag tgacgacact gacttctgcg 240
cattcgttta tacatgcata ttcttcaaaa ggatgcttct gccacttctc tttttcagtg 300
gctttcagtt caagaaaccc cattaatttc aaaagagaaa gcaggtggct atctgcacgg 360
aagaatggtc tcattgttct atttaagcat ttcctttttt cattgcacgt gtggtctaga 420
agagtttttc ctttcctcat atgaagccaa aataccatgt ccgagtttca cataatacaa 480
aacatttccc aggaagaaaa tgttcccaga gaccacatga gttctcttga aatctttgaa 540
atttataacc ctgacccatg aaatcgggca agaaaaactg taatggcatc agcaggatgt 600
gaagagaatg gaggcggcgt acacctaatg cggttttacc gagtcggata tggttgtcgt 660
atggacaaca ggctgttgat ttggtaagtg tcggattttt tagggagaca aaagtccaac 720
ctatccccaa gcaaatccgg ggaattcgat ggtctcttga atatgtaaat gcttttgaac 780
ttcagtgact gagtccaaat gatcttcttc ttctgcaagc taactaacct tcggtccttc 840
tcttggctgc tttttgcaac tactactata ttattgcttt tagtaatggt ggtagttgca 900
atagaagtaa gcatagtgaa aaagtgttga tcggcaacaa acaaagaagc ttaattatta 960
ccgatccagc acaccttaat catctccaac tgttctctat tcttgcatct tcaaccgtaa 1020
tcagcagata atcctcgtca ttaatcatta ttctgaaaca acctgttgcc ccaccaaaga 1080
aaactcatag gtgactctgc tttgttctct tgcaatgcca tatatacacc tgaaattctg 1140
atcgctctca ctcatctgtc gcattcaaag cctcaaagcc gcttgtttct tgaactttgc 1200
cttggcttca aagaagaaag tcctcaaata gaagatcgac catatgggac tgaagatatt 1260
ctcagtcggc tttgctcttc tttgttgctt ctgttcactt ggcttctgtg atcaagacgg 1320
ttttctgagt ttagcttgtg gtggaactac caattacacg gattcatcca acatctggtg 1380
gattaccgac agtgatttca taagcacagg aaagactacc tatgttgaca atatcgaggg 1440
caattcatct ggtgtttcgc ttcggttctt cccagattcc aaagtccat 1489

<210> 126
<211> 1273
<212> DNA
<213> Eucalyptus grandis

<400> 126
ttgtaaatta tgtgtgctta atagggtctt gttaatcaat gatcagtgta ttttttacgc 60
atgtgatgaa aaagtaattg cttttgagaa tatagttaca tcgaaaggac aatcaattcg 120
tttgacattg taatttttta tttgatagtt taacaagtgc ctcggaacac tcttcaacat 180
atcctttcac tttattttgc atatttatgc ttgtacaaca acattttcaa ttgggtgatc 240
ataattcgta atatttataa ttttttgtta acaatgagta actctatact cctggattga 300
gcaaacatat ttgtaaagta gttatgagag tattacttat acttagacgt tgtgagatac 360
tcatgatcgt atcatatgtc cactagagga tatagattta cctagatgaa gccccttttct 420
tagaagtagg aaaaaaaaaa ctattatatt gacttgaacc catatcataa aaagtacgag 480
actcaaaatc caatcttaca tgtatatgtg tatatatata tgttcgcaaa tgataacaat 540
cttttcaaga atcaagacac cagaaaacca tattttcaat atccgtcaat gtcaatgtcc 600
tactcacatc gaacaggact gccgcgtaca caacaagttc ccccagctaca gatttaccta 660
caattaggaa atgcaacccg aaaagacagg tctccatttc ttccttcact ttcccactca 720
tgaaaatgaa atatataatc acaaaatgcc tgagcgacac taaaggaacc aaagaacaac 780
gattccaact cagagagaga gagagagaga gagagaggca ctaatttttg gctgctcaac 840

aaaggaagca actttattca aatccatttt gctttagcgt gcccgtaatt ccaaccaaac 900
atatcctcaa agccctaata tatactccca caagcgcacc tcgtttccta cacacaagta 960
caaagcgtca acttcttctt cgctaaactg gtctcacaga cactcgcttg tccctcagtc 1020
cacactttgg cttagctcac agcaactatg gctgagacag cggaacccca gaagctggtc 1080
gagctcgaga aggtgcccga ccccgaggcc ggcgtgcccc cgaaaggaga ggaggcgccc 1140
ccagaacccc cacttccgcc cccagtgccg gcgccgccgg tggaaacttg cgtcttggtt 1200
gacgtggcac ttagggtttt gctcttcgca gcgacactga ccgctgtggt ggtgatggtc 1260
acggcgaacc aaa 1273

<210> 127
<211> 3720
<212> DNA
<213> Eucalyptus grandis

<400> 127
cgaagttcag ctcccgcttc cctgatgttt tcaaatcttc tttcaagtta gaagtacata 60
tacagcaaac aagatccaac ccttttctta tcatgagccc ttacttccac aagtgacatt 120
tggcactagt cccacaattt aatcattcta tttccattct ctgtaaatgt accctattca 180
aagttgggac ataatgaccc ttttgaagcg ttaggatcac actttattaa aagggaacaa 240
caacattgac agcaaatgca cgcactttcg ataaagttca gacagtataa taagttctca 300
ttccaaaagg ccccaatgtg gaaggtacga cttctctaac cctgttttga tttgattttt 360
tcgcagagga aaaatcatca ccaaagactt ataaaaattg aagtagcaaa gaaaagaaaa 420
gcaagattag caaacagaga ggagaaagag aggggaagga gtgatgggcc aacagccatt 480
ctcccagaaa ccacataaaa aacaaacaca gaatgatcac ttgtgaagaa cacgcggagt 540
tccaagcaaa gcatctcgag aatcaatgtc gctctttctt cacaagcatt ggacagaaaa 600
aaagagcaag ctctaagttt tccagcgaaa gcccgaaaat taggacgaag ggcgacgaga 660
aaacgaaaaa ctagaaggaa acaaaaatca aaataaaaag gaaagagagg cctgtgcgag 720
taataacgat tgtaaggcaa gacgatgaac cggcaaagct tgattcctgg ttgcaaattg 780
gggacgaaga tggctcaaaa taggagtgac gggcggtgat tttaccgcga agcgaaacct 840
agaatgcaag gagcaaagaa gagggtggtg gcagaatcga cgccgacagt ggcagcagag 900
tcgacgccag cagcagcggc ggagtgtatg agcggagaag gcgtagtagc tgatggtggt 960
ggagtcgaca agaggagaag gcaagaagga agagtcgtcc ggaaccaatg tgtttggctt 1020
tgggtgtgga tgttttgtat tttggtgaga tgagagaacg tgtttgtttc attgtttaag 1080
attaataatg tgttcacgag ccgaacaatg tttcgacctt aacccgactc aaaacatggt 1140
tgtttgcttg ttttgtaatt gttacctaaa taatattaag acctaaaaca tcgtgttcgg 1200
gttgagtttt tggacactcc tacctgtgat agccaccgcg agcgtagact actggatttg 1260
atatttggaa gcacgaccac cttttattgc caattggaaa gataaaaacg aggcacgaat 1320
gggaccaaaa tgagcaagaa atacggtatc tttggatgcc atgtttgcca tttgtcacct 1380
tacgcagagt gctagtgtaa attctcaatc aaagagcacg ggatacgttt tgttcagaac 1440
ttcacaccat gagcaggctt ggaaaaggag gaccgtaaag gaaatcacca tattgtagat 1500
gttcaaaata agttaacgaa tcagaaaaag aatacccatt tagccgaatt taattaacgt 1560
aatctttacg tgggacaact aaagtggaaa ttttttttaac ttgtgctgat gttttagctt 1620
taaaatgcaa tcaccagcct aaaatatatc ttgattcatt atttgaaatc tcgaatgtaa 1680
attttagtag tatatcataa atatctccgt ttggcctact ttctaatgca gcatccgttt 1740
gatagggtgt cgacgactca actctacgta cgtaaaaaaa aaaaattaaa aaatgccata 1800
ttgactttat agtgtagcac gtcatcaaat tgggcgagca gtcgtcggat ggaattaaaa 1860
ttacatcaaa tggaaattgt ttgttggttg cactttgggt caatttttt tggactttga 1920
tgtaagtaat taagttaagt aatgatttcc attcactagg aagtcgaagc ccacacaacc 1980
ttgaaaaaaa aaaaaaaaaa agacatcagt ccatgcaaac aacgaattaa ctgaatttaa 2040
tgaagaatac gagaaacgta aaaacttgat aagtttatta aacgatagga atgacattta 2100
gattaatgta agtacaagta tctatagaga gttatacaaa tatatatata tatatatata 2160
tatatataat atttcagata gttttatgaa aatacttaaa attaaataga agaaaaaata 2220
tcaaactgat attgctctaa atgggattct acttttacta tcatagagat aataagctaa 2280
ggtataatta agtagaacta tcgtaatata tataatatca ataagataaa aaagtaaata 2340
gaaagatagc cacttttttt gttattgagg aaatggattg aaatgaaata atattacgaa 2400
atcaacaata gtgatagaag gaatgatttg acctagttat ggaatatcga gtgactaaat 2460
caggcaaatc gaaagtttaa gaatttaggt tgcacattta gctatgttta aagaccatat 2520

tgtatctgtc atgatagttt agagacttgc gactctctct cttgcgcatt caaacaaaag 2580
aagaacaaaa aatttaagaa tgacgttgtg cactcggtca gagttaaaga actattagtg 2640
tgatttttc atttttaagt aaacaaaaca cgatgtggga gatgtgggag attggaaaag 2700
tgatggctaa aatttggaag aaaaatagaa atatgatcat gattgaagat ttataaaata 2760
aataatcatg gtacggactg aaactttaaa aaaatagtaa atgtactatg gtagacaaaa 2820
acaaattgag agtgtatatg gtaagggcaa cgctctttcc attccttata taactaaatt 2880
cacctaactc ttccaaaaat acaaagttgc atctatttta cattagtagt cccaaattta 2940
tttacttttt ttttttttag tttttatatc tacataagat ttacttacca tagttaagaa 3000
tttatatgtt taatttttagt taattttata ttttctatgt atattagagg cactatcttt 3060
cttttatccg ataatgcaat tttctttgat acgctaacaa acaaaacatg tgaaaagctt 3120
aattatggca attatcataa atagaaaaaa attagaaaaa aagagaggaa atgggccatt 3180
atttaaattg caatcgaaag attgagggca attctgtttc tctagtgtaa ataagggtgt 3240
atttaataat tgagggatgg aaatagcatg gtcactcggt aattatcaag gaaagcaaga 3300
ataaaaatgg aaaaaaaaaa aaaaaaagct tgaagaggcc aatgtcgaaa ttatgagcgc 3360
gagatgagga cactcctggg aaacgaaaaa tggcattcgc ggggggtgct atataaagcc 3420
tcgtgtaagg gtgcgttcct cactctcaaa ccctaatcct gcccttcccc tctgctgctg 3480
ctgctcgtca cctctctcct ccctctcgcg gccagctgcg agatctgccg agtttaagcc 3540
tcgtacatca aaatgggtaa ggagaagatt cacatcagca ttgtggtcat tggccatgtc 3600
gattctggga agtcaaccac aactggccac ttgatataca agctcggagg aatcgacaag 3660
cgtgtgattg agagattcga gaaggaagct gctgagatga acaagagatc gttcaagtat 3720

<210> 128
<211> 25
<212> DNA
<213> Eucalyptus grandis

<400> 128
tgagcggata acaatttcac acagg 25

<210> 129
<211> 25
<212> DNA
<213> Eucalyptus grandis

<400> 129
tcgagttttt tgatttcacg ggttg 25

<210> 130
<211> 54
<212> PRT
<213> Pinus radiata

<400> 130
Met Ala Thr Ala Thr Phe Ile Asp Ile Leu Leu Ala Ile Leu Leu Pro
1 5 10 15
Pro Leu Gly Val Phe Leu Lys Tyr Glu Cys His Ser Glu Phe Trp Ile
20 25 30
Cys Val Leu Leu Thr Leu Leu Gly Trp Leu Pro Gly Ile Ile Tyr Ala
35 40 45
Val Tyr Ile Leu Thr Lys
50

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ01/00115

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. [7]: C12N 15/11 C12N 15/29 A01H 1/00 A01H 5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
SEE ELECTRONIC DATABASES

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
SEE ELECTRONIC DATABASES

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
DGENE, EMBL, GENBANK, SWISS PROTEINS, PIR as per sequence ID Nos specified in inventions 1-5, 12, 20, 23, 30, 33, 36, 37, 39, 45, 46 as stated on extra sheets (1)-(4).

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P/X	GenBank Accession No. AR148900. 8 August 2001. See whole document. Also, US6225529 A (PIONEER HI BRED INT) 1 May 2001 See Seq ID 4.	1, 5-17, 23, 24 (Seq ID 59)
P/X	WO 0058474 A (GENESIS RESEARCH AND DEVELOPMENT CORPORATION LIMITED) 5 October 2000. See Table 1 and sequence listing.	1-24 (Seq ID 1-112, 117)
X	GenBank Accession No. AJ012552 (VFA012552). 13 November 1998. See whole document.	2, 3, 5, 9-17 (Seq ID 1)

[X] Further documents are listed in the continuation of Box C [X] See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search
12 September 2001

Date of mailing of the international search report
19 SEPTEMBER 2001

Name and mailing address of the ISA/AU

AUSTRALIAN PATENT OFFICE
PO BOX 200, WODEN ACT 2606, AUSTRALIA
E-mail address: pct@ipaustralia.gov.au
Facsimile No. (02) 6285 3929

Authorized officer

Terry Moore
Telephone No : (02) 6283 2632

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ01/00115

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank Accession No. L41658 (SCFPOLY). 28 November 1995. See whole document. Also, Albert, H.H. *et al.* 1995. Nucleotide sequence of sugarcane polyubiquitin cDNA. Plant Physiology. 109(1):337-337.	2, 3, 5, 9-17 (Seq ID 34)
X	GenPept Accession No. AAB21993. 7 May 1993. See whole document. Also, Christensen, A.H. *et al.* 1992. Maize polyubiquitin genes: structure, thermal perturbation of expression and transcript splicing, and promoter activity following transfer to protoplasts by electroporation. Plant Molecular Biology. 18(4):675-689.	4 (Seq ID 67)
X	GenPept Accession No. AAA68878. 23 June 1995. See whole document. Also, Callis, J. *et al.* 1995. Structure and evolution of genes encoding polyubiquitin and ubiquitin-like proteins in *Arabidopsis thaliana* ecotype Columbia. Genetics. 139(2):921-939.	4 (Seq ID 80)
X	EMBL Accession No. D10851 (ATHCDC2BG). 14 April 2000. See whole document. Also, Imajuku, Y. *et al.* 1992. Exon-intron organization of the *Arabidopsis thaliana* protein kinase genes CDC2a and CDC2b. FEBS Letters. 304:73-77.	1, 5-17, 23, 24 (Seq ID 4)
X	EMBL Accession No. U12012 (PTU12012). 23 March 1996. See whole document. Also, Voo, K.S. *et al.* 1995. 4-coumarate:coenzyme a ligase from loblolly pine xylem. Isolation, characterisation, and complementary DNA cloning. Plant Physiology. 108(1):85-97.	1, 5-17, 23, 24 (Seq ID 6)
X	GenBank Accession No. AF139445. 1 June 1999. See whole document.	1, 5-17, 23, 24 (Seq ID 7, 8)
X P/X	Asamizu,E. *et al.* 1998. Structural analysis of *Arabidopsis thaliana* chromosome 5. VIII. Sequence features of the regions of 1,081,958 bp covered by seventeen physically assigned P1 and TAC clones. DNA Research. 5(6):379-391. Also, GenBank Accession No. AB016885. 27 December 2000 See whole document.	1,5-17,23,24 (Seq ID 20)
X	SWISS-PROT Accession No. O24493 (MC1_PINRA). 15 July 1999.	4 (Seq ID 73-75)
X	GenBank Accession No. AF075270. 24 September 1998. See whole document.	1, 5-17, 23, 24 (Seq ID 30)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ01/00115

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank Accession No. X61915 (PTCABP). 23 November 1998. See whole document. Also, Kojima, K. *et al.* 1992. Structure of the pine (*Pinus thunbergii*) chlorophyll a/b-binding protein gene expressed in the absence of light. Plant Molecular Biology. 19(3):405-410.	1, 5-17, 23, 24 (Seq ID 2, 3, 94)
X	GenBank Accession No. U53418 (GMU53418). 28 May 1997. See whole document. Also, Tenhaken, R. *et al.* 1996. Cloning of an enzyme that synthesizes a key nucleotide-sugar precursor of hemicellulose biosynthesis from soybean: UDP-glucose dehydrogenase. Plant Physiology. 112(3):1127-1134.	1, 5-17, 23, 24 (Seq ID 115)
X	GenBank Accession No. Z14990 (ATUBC9). 18 May 1993. See whole document. Also, Girod, P.A. *et al.* 1993. Homologs of the essential ubiquitin conjugating enzymes UBC1, 4, and 5 in yeast are encoded by a multigene family in *Arabidopsis thaliana*. Plant Journal. 3 (4):545-552.	14-17 (Seq ID 50)
X	Walden, A.R. *et al.* 1999. Genes expressed in *Pinus radiata* male cones include homologs to anther-specific and pathogenesis response genes. Plant Physiology. 121(4):1103-1116. Also	1, 3, 5-17, 23, 24 (Seq ID 51, 52, 53, 112)
P/X	GenBank Accession No. U90350 (PRU90350). 17 October 2000. See whole document.	
X	EMBL Accession No. D63396 (NTBY2A, TOBBY2A). 13 February 1999. See whole document. Also, Kumagai F. *et al.* 1995. The involvement of protein synthesis elongation factor 1a in the organization of microtubles in the perinuclear region during the cell cycle transition from M phase to G1 phase in tobacco BY-2 cells. Bot. Acta. 108:467-473.	1, 3, 5-17, 23, 24 (Seq ID 61)
X	GenPept Accession No. AAD56019 (AF181491_1). 22 September 1999. See whole document.	4 (Seq ID 79)
X	GenBank Accession No. X74814 (EGOMTRN). 22 September 1994. See whole document. Also, Poeydomenge,O. *et al.* 1994. A cDNA encoding S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase from *Eucalyptus*. Plant Physiology. 105(2):749-750.	1, 5-17, 23, 24 (Seq ID 113)
X	GenBank Accession No. X53043 (LEEF1A). 9 May 1995. See whole document. Also, Curie, C. *et al.* 1992. The activation process of *Arabidopsis thaliana* A1 gene encoding the translation elongation factor EF-1 alpha is conserved among angiosperms. Plant Molecular Biology. 18(6):1083-1089.	1, 5-17, 23, 24 (Seq ID 127)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ01/00115

Box I **Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos :
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos :
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II **Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

The international application does not comply with the requirement of unity of invention because it does not relate to one invention only or to a group of inventions so linked as to form a single general inventive concept.
(continued on extra sheet 1)

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically:

Three (3) additional search fees were paid resulting in a total of 15 inventions being searched as follows:
Inventions: 1-5, 12, 20, 23, 30, 33, 36, 37, 39, 45 and 46 as stated on the extra sheets (1)-(4).

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

Supplemental Box
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (extra sheet 1)

The international application has claimed nucleic acid sequences of 46 different regulatory regions, their use in modifying endogenous and/or heterologous gene expression and the phenotypes of plants resulting from this gene expression. Also claimed are coding regions relating to several of the regulatory regions.

The nucleic acid sequences and their putative amino acid sequences have been shown to have a similarity to promoters that are known to be involved in the regulation of transcription and/or expression in plants (p.6 Lines 25-32 and Table 1). Based on this methodology, sequences 1-14, 20 and 22-127 have been assigned with 46 different regulatory activities. However, these regulatory regions and proteins are not unified by a sequence homology or by a common gene upon which they act. Plant promoters generally have been known in the art for some time and indeed many of the promoters referred to in Table 1 have previously been identified and used (refer to citations listed in Box C). Therefore, the use of the nucleotide sequences identified as promoters to modulate transcription in plants does not constitute a special technical feature under Rule 13.2.

The International Searching Authority has found that there are 46 separate inventions, wherein a single promoter or transcription modulator provides the special technical feature; they are listed below:

1. Nucleic and amino acid sequences SEQ ID NOs 1-3, 34, 67, 80 and their at least 40% identical homologues encoding super ubiquitin and regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
2. Nucleic acid sequence SEQ ID NO 4 and its at least 40% identical homologues encoding a cell divisional control regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
3. Nucleic acid sequence SEQ ID NO 5 and its at least 40% identical homologues encoding a xylogenesis specific regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
4. Nucleic acid sequence SEQ ID NO 6 and its at least 40% identical homologues encoding a 4-Coumarate-CoA Ligase regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
5. Nucleic acid sequences SEQ ID NOs 7, 8, 20 and their at least 40% identical homologues encoding cellulose synthase regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
6. Nucleic acid sequences SEQ ID NOs 9-11 and their at least 40% identical homologues encoding leaf specific regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
7. Nucleic and amino acid sequences SEQ ID NOs 12, 60, 78 and their at least 40% identical homologues encoding O-methyl transferase regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
8. Nucleic acid sequences SEQ ID NOs 13, 14, 126 and their at least 40% identical homologues encoding root specific regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
9. Nucleic and amino acid sequences SEQ ID NOs 22, 63 and their at least 40% identical homologues encoding pollen coat protein regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

(continued on extra sheet 2)

Supplemental Box
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (extra sheet 2)

10. Nucleic and amino acid sequences SEQ ID NOs 23-25, 64 and their at least 40% identical homologues encoding pollen allergen regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
11. Nucleic and amino acid sequences SEQ ID NOs 26-28, 65, 66 and their at least 40% identical homologues encoding auxin induced protein regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
12. Nucleic acid sequences SEQ ID NOs 29-33, 59, 89, 90 and their at least 40% identical homologues encoding flower specific regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
13. Nucleic and amino acid sequences SEQ ID NOs 35, 39, 68, 93 and their at least 40% identical homologues encoding glyceraldehyde-3-phosphate dehydrogenase regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
14. Nucleic and amino acid sequences SEQ ID NOs 36 and 69 and their at least 40% identical homologues encoding carbonic anhydrase regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
15. Nucleic acid sequences SEQ ID NOs 37, 38 and their at least 40% identical homologues encoding isoflavone reductase regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
16. Nucleic and amino acid sequences SEQ ID NOs 40, 70 and their at least 40% identical homologues encoding bud specific regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
17. Nucleic acid sequences SEQ ID NOs 41-44, 92 and their at least 40% identical homologues encoding xylem specific regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
18. Nucleic and amino acid sequences SEQ ID NOs 45, 71 and their at least 40% identical homologues encoding meristem specific regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
19. Nucleic and amino acid sequences SEQ ID NOs 46-48, 72 and their at least 40% identical homologues encoding senescence like protein regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
20. Nucleic and amino acid sequences SEQ ID NOs 49-53, 73-75, 94 and their at least 40% identical homologues encoding pollen specific regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
21. Nucleic acid sequences SEQ ID NOs 54, 55 and their at least 40% identical homologues encoding nodulin homolog pollen specific regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.
22. Nucleic and amino acid sequences SEQ ID NOs 56-58, 76, 77, 91 and their at least 40% identical homologues encoding sucrose synthase regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

(continued on extra sheet 3)

Supplemental Box
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (extra sheet 3)

23. Nucleic and amino acid sequences SEQ ID NOs 61, 62, 79 and their at least 40% identical homologues encoding elongation factor A regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

24. Nucleic and amino acid sequences SEQ ID NOs 81-86, 87 and their at least identical 40% homologues encoding MIF homologue regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

25. Nucleic acid sequence SEQ ID NO 88 and its at least 40% identical homologues encoding a chalcone synthase regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

26. Nucleic acid sequences SEQ ID NOs 95, 96 and their at least 40% identical homologues encoding *Pinus radiata* male specific protein regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

27. Nucleic acid sequences SEQ ID NOs 97, 114 and their at least 40% identical homologues encoding UDP glucose glycosyltransferase regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

28. Nucleic acid sequences SEQ ID NOs 98, 99 and their at least 40% identical homologues encoding elongation factor A1 regulatory and coding regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

29. Nucleic acid sequences SEQ ID NOs 100-102 and their at least 40% identical homologues encoding S-adenosylmethionine synthetase regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

30. Nucleic acid sequences SEQ ID NOs 103, 115 and their at least 40% identical homologues encoding UDP glucose-6-dehydrogenase regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

31. Nucleic acid sequences SEQ ID NO 104 and its at least 40% identical homologues encoding a hypothetical protein regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

32. Nucleic acid sequences SEQ ID NOs 105, 106, 116 and their at least 40% identical homologues encoding laccase 1 regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

33. Nucleic acid sequences SEQ ID NOs 107, 117 and their at least 40% identical homologues encoding arabinogalactan-like 1 regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

34. Nucleic acid sequences SEQ ID NOs 108, 109 and their at least 40% identical homologues encoding arabinogalactan-like 2 regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

35. Nucleic acid sequences SEQ ID NOs 110, 111 and their at least 40% identical homologues encoding root receptor-like kinase regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

(continued on extra sheet 4)

Supplemental Box
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (extra sheet 4)

36. Nucleic acid sequence SEQ ID NO 112 and its at least 40% identical homologues encoding a *Pinus radiata* lipid transfer protein 2 regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

37. Nucleic acid sequence SEQ ID NO 113 and its at least 40% identical homologues encoding a caffeic acid O-methyltransferase regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

38. Nucleic acid sequence SEQ ID NO 118 and its at least 40% identical homologues encoding a constans regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

39. Nucleic acid sequence SEQ ID NO 119 and its at least 40% identical homologues encoding a flowering promoting factor 1 regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

40. Nucleic acid sequence SEQ ID NO 120 and its at least 40% identical homologues encoding an agamous regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

41. Nucleic acid sequence SEQ ID NO 121 and their at least 40% identical homologues encoding a dreb 1A transcription factor regulatory , DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

42. Nucleic acid sequence SEQ ID NO 122 and their at least 40% identical homologues encoding a drought induced protein 19 regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

43. Nucleic acid sequence SEQ ID NO 123 and its at least 40% identical homologues encoding a salt tolerance protein regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

44. Nucleic and amino acid sequences SEQ ID NOs 124, 130 and their at least 40% identical homologues encoding low temperature induced LTI-16 coding and regulatory regions, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

45. Nucleic acid sequence SEQ ID NO 125 and its at least 40% identical homologues encoding a xylem specific receptor-like kinase regulatory region, DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

46. Nucleic acid sequence SEQ ID NO 127 and its at least 40% identical homologues encoding an elongation factor 1-alpha regulatory , DNA constructs including same and methods of modulating transcription, expression and phenotype in plants using these sequences.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/NZ01/00115

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member	
US	6225529	US	6020162
WO	00/58474	AU	00/27024

END OF ANNEX